

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2004, 10:53:58 ; Search time 2808 Seconds  
(without alignments)  
5721.458 Million cell updates/sec

Title: US-09-782-745-14

Perfect score: 538

Sequence: 1 ACGCCAGGAGCTGTGAGGC.....CTGCAAGAAAAA 538

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 28520704

Minimum DB seq length: 0

Maximum DB seq length: 538

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	513	95.4	537	12	BM832793	BM832793 K-EST0107
2	492	91.4	527	12	BI826605	BI826605 603077056
3	491.2	91.3	521	13	EX108227	EX108227 BX108227
4	485.8	90.3	517	14	CF780547	CF780547 AGENCOURT

5	476.8	88.6	509	12	BI868671	BI868671 603392594
6	452.4	84.1	489	9	AA447559	AA447559 zw81e11.s
7	431.4	80.2	457	10	AW510753	AW510753 hd39d05.x
8	424.6	78.9	447	9	AI381509	AI381509 te76b07.x
9	424.4	78.9	464	9	AA738037	AA738037 nx15e11.s
10	415.2	77.2	505	14	CB115693	CB115693 K-EST0159
11	413.8	76.9	418	9	AW016546	AW016546 UI-H-Biop
12	413.4	76.8	480	12	BG120336	BG120336 602353732
13	412.8	76.7	426	9	AA868226	AA868226 ak48h07.s
14	410.8	76.4	450	9	AA760996	AA760996 dx32h08.s
15	401.2	74.6	455	9	AI187350	AI187350 qf29a05.x
16	365.4	67.9	412	9	AW102587	AW102587 xd67907.x
17	360.4	67.0	445	11	BC005363	BC005363 Homo sapi
18	359.4	66.8	419	9	AA448542	AA448542 zw81e11.r
19	357	66.4	383	12	BM836228	BM836228 K-EST0111
20	335.2	62.3	341	12	BP431265	BP431265 BP431265
21	329.8	61.3	384	9	AA913206	AA913206 op53f03.s
22	322.4	59.9	383	13	BX283580	BX283580 BX283580
23	318.8	59.3	397	12	BG206349	BG206349 RST25797
24	307.2	57.1	333	13	BUS33718	BUS33718 AGENCOURT
25	296.4	55.1	398	9	AA918604	AA918604 ol53f02.s
26	290.6	54.0	320	12	BM836021	BM836021 K-EST0111
27	269.8	50.1	275	14	CB147043	CB147043 K-EST0202
28	269.8	50.1	275	14	CB150355	CB150355 K-EST0207
29	269.8	50.1	275	14	CB157288	CB157288 K-EST0216
30	253.8	47.2	457	14	CF780497	CF780497 AGENCOURT
31	250.4	46.5	256	12	BG181480	BG181480 RST328 At
32	233.4	43.4	258	12	BG186708	BG186708 RST5683 A
33	228.2	42.4	253	12	BG184057	BG184057 RST2973 A
34	226.6	42.1	261	12	BG199060	BG199060 RST18338
35	224.8	41.8	245	12	BG212621	BG212621 RST32216
36	219.8	40.9	245	12	BG212622	BG212622 RST32217
37	214.8	39.9	292	12	BG208433	BG208433 RST27934
38	213.4	39.7	524	11	AF318372	AF318372 Homo sapi
39	207.6	38.6	507	9	AA972716	AA972716 op90e12.s
40	207	38.5	256	12	BG216461	BG216461 RST36040
41	207	38.5	520	14	CB961487	CB961487 AGENCOURT
42	204.8	38.1	224	9	AA738394	AA738394 nx28c12.s
43	202.4	37.6	382	10	BF869799	BF869799 IL3-ET011
44	200.6	37.3	499	12	BG354572	BG354572 PLAC6 Hum
45	193.8	36.0	197	9	AI968311	AI968311 wd01f07.x

#### ALIGNMENTS

RESULT 1	BM832793	537 bp	mRNA	linear	EST 06-MAR-2002			
LOCUS	K-EST0107334	S5SNU484s1	Homo sapiens	cdna clone	S5SNU484s1-8-F10			
DEFINITION	5', mRNA sequence.							
ACCESSION	BM832793							
VERSION	BM832793.1	GI:19189202						
KEYWORDS	EST.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE	1 (bases 1 to 537)							

FEATURES  
source

Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S55NU484s1-8-F10"  
/sex="M"  
/tissue\_type="Stomach"  
/cell\_type="Epithelial"  
/cell\_line="SNU-484"  
/lab\_host="Top10F"  
/clone\_lib="S55NU484s1"  
/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;  
Site 2: NotI. The poly (A)+ RNA was decapped with tabacco  
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker  
including EcoRI site by treatment of T4 RNA ligase. The  
first strand cDNA was synthesized from oligo dt-selected  
mRNA by priming with dt-tailed vector. The dt-tailed  
vector was adjusted to have about 60nt. The cDNA vector  
was circularized with E. coli DNA ligase after digestion  
of EcoRI which site is also included in vector. An RNA  
strand converted to a DNA strand by Okayama-Berg method.  
The obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F by electroporation method.  
After analyzing and sequencing about 2,000 ~ 3,000  
colonies in original cDNA library, the abundant cDNAs were  
selected and amplified by PCR reaction using vector region  
primer including T7 promotor as 5' primer and N(dR)14 as  
3' primer. The PCR products were used as template for  
synthesis of biotinylated single stranded RNA by in vitro  
transcription reaction. The synthesized RNA probes were  
hybridized with antisense single stranded cDNAs prepared  
from original library and incubated with avidin-gel.  
After removing DNA-RNA hybrids by centrifuge, the  
subtracted cDNA libraries were constructed by  
transformation of the remaining DNA into competent cells E.  
coli Top10F with electroporation method."

## ORIGIN

Query Match 95.4%; Score 513; DB 12; Length 537;  
Best Local Similarity 98.5%; Pred. No. 3.4e-105;  
Matches 529; Conservative 0; Mismatches 5; Indels 3; Gaps 1;  
  
QY 3 GCCAGGAGCTGTGAGGAGCTGTGTTCTCGCGTCCGACTCTTTTCTCTAC 62  
DB 1 GCCAGGAGCTGTGAGGAGCTGTGTTCTCGCGTCCGACTCTTTTCTCTAC 60  
  
QY 63 TGAGATTTCATCTGTGAAATATGAGTTGGCGAGGAGATCGACC---TATCGGCTTGA 119  
DB 61 TGAGATTTCATCTGTGAAATATGAGTTGGCGAGGAGATCGACCATTATTGGCTTGA 120  
  
QY 120 CCAAGACCTACGTAGACCTCTGAATGATTTGGGCTATGCGGCCGAGCAGTTCAGT 179  
DB 121 CCAAGGCGCTATGTACAGCTCTTGAAGTGTATGGGCTATGCGGCCGAGCAGTTCAGT 180  
  
QY 180 GATGAAGTGAACACAGCAACCTCAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 239  
DB 181 GATGAAGTGAACACAGCAACCTCAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 240  
  
QY 240 GCAGCTGCTCAGGAGGAGAGGATGAGGAGATCTGCAGGTCAGAGGCGGAGGCTGAA 299  
DB 241 GCAGCTGCTCAGGAGGAGAGGATGAGGAGATCTGCAGGTCAGAGGCGGAGGCTGAA 300  
  
QY 300 GCTCATACCCAGGACAGGTCACCCAGAGCTGGTGTGAGTGTGAAGATGGTCTCAT 359  
DB 301 GCTCATACCCAGGACAGGTCACCCAGAGCTGGTGTGAGTGTGAAGATGGTCTCAT 360  
  
QY 360 GGGCAGGAGATGGAACCCGCAAAATCCAGAGGAGGTGAAACCGCTGAAGAGGTGAAAG 419  
DB 361 GGGCAGGAGATGGAACCCGCAAAATCCAGAGGAGGTGAAACCGCTGAAGAGGTGAAAG 420  
  
QY 420 CAATCACAGTGTAAAAAGAGACAGTTGAATGATGAGGCTGCTCTATGTTGAAT 479  
DB 421 CAATCACAGTGTAAAAAGAGACAGTTGAATGATGAGGCTGCTCTATGTTGAAT 480

## Db

421 CAATCACAGTGTAAAAAGAGACAGTTGAATGATGAGGCTGCTCTATGTTGAAT 480  
QY 480 TTGTTTCATTAAAAATCTCCCAATAAAGCTTTTACAGCTTTCTCAAGAAAAA 536  
DB 481 TTGTTTCATTAAAAATCTCCCAATAAAGCTTTTACAGCTTTCTCAAGAAAAA 537

## RESULT 2

BI826605  
LOCUS BI826605  
DEFINITION 60307056F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:516892 5',  
mRNA sequence.

ACCESSION BI826605  
VERSION BI826605.1 GI:15938155  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 527)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgaps-f@mail.nih.gov](mailto:cgaps-f@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L14M11419 row: p column: 13

High quality sequence stop: 519.

## FEATURES

source

Location/Qualifiers

1. .527

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:516892"

/tissue\_type="medulla"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH\_MGC Library."

## ORIGIN

Query Match 91.4%; Score 492; DB 12; Length 527;  
Best Local Similarity 98.3%; Pred. No. 1.8e-100;  
Matches 519; Conservative 0; Mismatches 5; Indels 4; Gaps 2;  
  
QY 12 CTGTGAGGACGTGCTGTGTGTTCTCTCGCGTCCGAGCTCTTTTCTCTACTGATTC 71  
DB 1 CTGTGAGGACGTGCTGTGTGTTCTCTCGCGTCCGAGCTCTTTTCTCTACTGATTC 60  
  
QY 72 TCTGTGTGAATATGAGTTGGCGAGGAGATCGACC---TATCGGCTTAGACCAAGCGC 128  
DB 61 TCTGTGTGAATATGAGTTGGCGAGGAGATCGACCATTATTATTTGGCTTAGACCAAGCGC 120  
  
QY 129 TACGTAGAGCTCTCTGAATGATTTGGGCTATGGGCCGAGCAGTTCAGTGATGAAGTG 188  
DB 121 TATGTACAGCTCTCTGAATGATTTGGGCTATGGGCCGAGCAGTTCAGTGATGAAGTG 180  
  
QY 189 GAACCAAGCAACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGGATCTCTGCACTGCT 248  
DB 181 GAACCAAGCAACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGGATCTCTGCACTGCT 240

QY 249 CAGGAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAAGCTCATAGC 308  
 Db 241 CAGGAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAAGCTCATAGC 300  
 QY 309 CAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCGAGGAG 368  
 Db 301 CAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCGAGGAG 360  
 QY 369 ATGACCCCGCAATCCAGAGGAGGTCAAAACCCCTGAAGAGGTGAAGAAGCAATCACAG 428  
 Db 361 ATGACCCCGCAATCCAGAGGAGGTGAAGAGGTGAAGAAGCAATCACAG 420  
 QY 429 TGTTAAAGAGACAGCTTGAATATGATGAGAGGTGCTCTATCTTGAAGATTTGTCATT 488  
 Db 421 TGTTAAAGAGAGGACAGCTTGAATATGATGAGAGGTGCTCTATCTTGAAGATTTGTCATT 480  
 QY 489 AAAATTTCTCCCAATAAGCTTTACAGCTTCTGCAAGAAAAA 536  
 Db 481 AAAATTTCTCCCAATAAGCTTTACAG-CTTCTGCAAGAAAAA 527

RESULT 3  
 BXL08227  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 521)  
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
 Radloff, U., Schneider, D. and Korn, B.  
 Human Unigeneset - RZPD3  
 Unpublished (2003)  
 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGp998K213161.  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de

This clone is available royalty-free from RZPD;  
 contact RZPD (clonerzpd.de) for further information. Seq primer:  
 M13r, Primer sequence: TTTCACAGCAAGACAGCTATGAC.

## FEATURES

source

Location/Qualifiers  
 1..521  
 /organism="Homo sapiens"  
 /mol\_type="cDNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGp998K213161 ; IMAGE:1256204"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP GC3"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; 1st strand cDNA was prepared from 3 pooled  
 germ cell tumors, and was then primed with a Not I -  
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified p773  
 vector. Library is not normalized. Library was  
 constructed by Bento Soares and M. Fatima Bernaldo."

## ORIGIN

Query Match 91.3%; Score 491.2; DB 13; Length 521;  
 Best Local Similarity 97.9%; Pred. No. 2.7e-100;  
 Matches 509; Conservative 0; Mismatches 8; Indels 3; Gaps 1;  
 QY 20 CAGTGTGTGTGTCTCTCGGCTCCGAGCTCTTTTCTCTACTGAGATTCACTGTGTG 79  
 Db 1 CAGTGTGTGTGTCTCTCGGCTCCGAGCTCTTTTCTCTACTGAGATTCACTGTGTG 60  
 QY 80 AAATATGAGTTGGCGAGGAGATCGACC--TATCGGCCTAGACCAAGACGCTACGTAGA 136  
 Db 61 AAATATGAGTTGGCGAGGAGATCGACCCTGTATTGGCCTAGTCCAAAGACGCTATGTACA 120  
 QY 137 GCCTCTGAAATGATTGGCCTTATGCGGCCGAGCAGATTCACTGATGAAGTGAACACAGC 196  
 Db 121 GCCTCTGAAATGATTGGCCTTATGCGGCCGAGCAGATTCACTGATGAAGTGAACACAGC 180  
 QY 197 AACACCTGAAGAGGGGAACCACTCAAGTCAAGTCAAGTCTGAGTCTGAGTCTGAGGAGG 256  
 Db 181 AACACCTGAAGAGGGGAACCACTCAAGTCAAGTCAAGTCTGAGTCTGAGTCTGAGGAGG 240  
 QY 257 AGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAAGCTCATAGCCAGCAACA 316  
 Db 241 AGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAAGCTCATAGCCAGCAACA 300  
 QY 317 GGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCTGATGGCGAGGATGGACCC 376  
 Db 301 GGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCTGATGGCGAGGATGGACCC 360  
 QY 377 GCCAATCCAGAGGAGGTGAAGAGCCTGAAGAGGTGAAGAGCAATCACTGTGTTAAA 436  
 Db 361 GCCAATCCAGAGGAGGTGAAGAGCCTGAAGAGGTGAAGAGCAATCACTGTGTTAAA 420  
 QY 437 GAAGCACGTTGAAATGATGAGGCTGCTCTATCTTGGAAATTTGTTCAATAAATTTCT 496  
 Db 421 GAAGCACGTTGAAATGATGAGGCTGCTCTATCTTGGAAATTTGTTCAATAAATTTCT 480  
 QY 497 CCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 536  
 Db 481 CCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 520

RESULT 4  
 CF780547  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 517)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: James Martin, University of Iowa  
 cDNA Library Preparation: M. Bento Soares, University of Iowa  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: NDAM604 row: e column: 12  
 High quality sequence stop: 517.  
 Location/Qualifiers

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

## FEATURES

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1. 517
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524555"
/tissue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_217"
/notes="Vector: pYX-Asc; Site 1: EcoRI; Site 2: NotI; Library is oligo-dT primed and directionally cloned. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to rRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. Average insert size 0.5-1kb. Adaptors 5' (AATCGGCACGAGG)3' and 5' d (CCTCGCGG)3'. 3' Linker sequence - GCGCGCGTCGAGGCC T18. Sequencing primers 3' end: T3 promoter primer 5' d (AATACCCCTCACTAAGGA)3'. 5' End: T7 promoter primer 5' d (TAATACGCTCACTAAGG)3'. Average insert size 0.5-1kb. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library."

source
ORIGIN
Query Match 90.3%; Score 485.8; DB 14; Length 517;
Best Local Similarity 98.1%; Pred. No. 4.5e-99;
Matches 503; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

QY 14 GTGAGGAGTCTGTGGTTCCTCGCGTCGGACTCTTTTCCTACTGAGATTCATC 73
DB 4 GAGGGGAGTCTGTGGTTCCTCGCGTCGGACTCTTTTCCTACTGAGATTCATC 63
QY 74 TGTGTAATATGATTTGGCAGGAAGATGAGC---TATCGGCTAGACCAAGCGCTA 130
DB 64 TGTGTAATATGATTTGGCAGGAAGATGAGCCTATTATTGGCTAGACCAAGCGCTA 123
QY 131 CGTAGAGCTCTGAAATGATGGCTATCGCGCCGAGCAGTTCAGTATGAAGTGA 190
DB 124 TGTACAGCTCTGAAATGATTTGGGCTTATCGCGCCGAGCAGTTCAGTATGAAGTGA 183
QY 191 ACCAGCACTGTAAGAAGGGGACCAAGCAACTCAACGTGAGGATCTCGAGCTGTCA 250
DB 184 ACCAGCACTGTAAGAAGGGGACCAAGCAACTCAACGTGAGGATCTCGAGCTGTCA 243
QY 251 GGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGCCGAGACGCTGAGCTATAGCA 310
DB 244 GGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGCCGAGACGCTGAGCTATAGCA 303
QY 311 GGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGTGTCTGATGGCAGGAT 370
DB 304 GGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGTGTCTGATGGCAGGAT 363
QY 371 GGACCCGCAATCCAGAGGAGGTGAAACCGCTGAAGAGGTGAAAGCAATCACAGT 430
DB 364 GGACCCGCAATCCAGAGGAGGTGAAACCGCTGAAGAGGTGAAAGCAATCACAGT 423
QY 431 TTAAGAAGACACCTTGAATGATGAGGCTGTCTTATGTTGAATTTCTTATTA 490
DB 424 TTAAGAAGACACCTTGAATGATGAGGCTGTCTTATGTTGAATTTCTTATTA 483
QY 491 AATTCCTCCATAAAGCTTTACAGCTTCTGCA 523
DB 484 AATTCCTCCATAAAGCTTTACAGCTTCTGCA 516

RESULT 5
BI868671
LOCUS 603392594F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5',
DEFINITION mRNA sequence.
ACCESSION BI868671
VERSION BI868671.1 GI:16042344

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LHAM12026 row: 1 column: 24
High quality sequence stop: 509.
Location/Qualifiers
1. 509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5402663"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 88.6%; Score 476.8; DB 12; Length 509;
Best Local Similarity 98.0%; Pred. No. 4.8e-97;
Matches 494; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

QY 1 ACGCCAGGAGCTGTGAGGAGTCTGTGGTTCCTCGCGTCGGACTCTTTTCTCT 60
DB 6 ACGTAGGAGCTGTGAGGAGTCTGTGGTTCCTCGCGTCGGACTCTTTTCTCT 65
QY 61 ACTGAGATTCATCTGTGTAATATGATTTGGCGAGGAAGATCGACC---TATCGGCCTA 117
DB 66 ACTGAGATTCATCTGTGTAATATGATTTGGCGAGGAAGATCGACCCTATTATTGGCCTA 125
QY 118 GACCAAGACGCTAGTAGGCTCTTGAATGATTTGGCCCTATGCGGCCGAGCAGTTCA 177
DB 126 GACCAAGGCGCTATGTACAGCTCTTGAATGATTTGGCCCTATGCGGCCGAGCAGTTCA 185
QY 178 GTGATGAGTGAACCAACAGCAACCTGAAGAGGGGAACCAAGCACTCAAGCTCAGGATC 237
DB 186 GTGATGAGTGAACCAACAGCAACCTGAAGAGGGGAACCAAGCACTCAAGCTCAGGATC 245
QY 238 CTGACAGTCTCTCAGGAGGAGGAGATGAGGAGCATCTGAGGTCAAGGCCGAGACCTG 297
DB 246 CTGACAGTCTCTCAGGAGGAGGAGATGAGGAGCATCTGAGGTCAAGGCCGAGACCTG 305
QY 298 AAGCTCATAGCAGGAGGAGTCAACCCACAGCTGGGTGTGAGTGTGAAGATGCTCTG 357
DB 306 AAGCTCATAGCAGGAGGAGTCAACCCACAGCTGGGTGTGAGTGTGAAGATGCTCTG 365
QY 358 ATGGGCGAGGATGGACCCGCAATCCAGAGGAGGTGAAACCGCTGAAGAGGTGAAA 417
DB 366 ATGGGCGAGGATGGACCCGCAATCCAGAGGAGGTGAAACCGCTGAAGAGGTGAAA 425
QY 418 AGCAATCAGTGTGTAAGAAGACACGTTGAATGATGCGGCTGCTCTATGTTGAA 477
DB 426 AGCAATCAGTGTGTAAGAAGACACGTTGAATGATGCGGCTGCTCTATGTTGAA 485
QY 478 ATTGTGTCATTAATAATTTCTCCCA 501
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```

Db      486 ATTGTTCAATAAAATCTCCAA 509
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RESULT 6
AA447559/c
LOCUS      489 bp      mRNA      linear      EST 04-JUN-1997
DEFINITION zw81e11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:782636
3' similar to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ; mRNA
sequence.
ACCESSION AA447559
VERSION    AA447559.1 GI:2161229
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 489)
AUTHORS    Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wyllie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
JOURNAL     Unpublished (1997)
COMMENT     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 427.
FEATURES             Location/Qualifiers
     source           1..489
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:782636"
                     /sex="male"
                     /lab_host="DH10B"
                     /clone_lib="Soares testis NHT"
                     /note="Vector: pT73p-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5]
TGTTACCAATCTGAAGTGGAGCGGCCCAATTTTTTTTTTTT 3'.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cots5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match      84.1%; Score 452.4; DB 9; Length 489;
Best Local Similarity 98.0%; Pred. No. 1.5e-91;
Matches 480; Conservative 0; Mismatches 6; Indels 4; Gaps 2;

QY 43 CCGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGTTGGCGAGGAAGAT 102
Db 489 CCGGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGTTGGCGAGGAAGAT 430
QY 103 CGACC---TATCGGCTAGACCAAGACGCTAGTAGCCCTCTGAAATGATTTGGGCTTA 159
Db 429 CGACTTATTTGGCCTTAGACCAAGGCGCTATGTACAGCCCTCTCTGAGTGATT-GGGCTA 371
QY 160 TGCGCCCGCGAGCTTCAGTGATGAAGTGGACCAAGCAACACCTGGAAGAGGGAACCG 219
Db 370 TGGCGCCCGAGCACTTCAGTGATGAAGTGGACCAAGCAACACCTGGAAGAGGGAACCG 311
QY 220 CAATCTAACGTCAGGATCTCTGAGTGTCTAGGAGGAGGAGGATGAGGAGCATCTGCAG 279
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Db      486 ATTGTTCAATAAAATCTCCAA 509
|||||
RESULT 7
AWS10753/c
LOCUS      457 bp      mRNA      linear      EST 03-MAR-2000
DEFINITION hd39d05.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2911881 3' similar to SW:GGS4_HUMAN Q13068 GAGE-4 PROTEIN. ;
mRNA sequence.
ACCESSION AWS10753
VERSION    AWS10753.1 GI:7148831
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 457)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40JP from Gibco.
FEATURES             Location/Qualifiers
     source           1..457
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2911881"
                     /lab_host="DH10B"
                     /clone_lib="Soares NFL T GBC S1"
                     /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
724808-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match      80.2%; Score 431.4; DB 10; Length 457;
Best Local Similarity 98.0%; Pred. No. 8.2e-87;
Matches 448; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

```

77 GTGAATATGAGTTGGCGAGGAGATCGACCTATC---GGCCTAGACCAAGAGCGTACGTT 133  
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457 GTGAATATGAGTTGGCGAGGAGATCGACCTATTAATTGGCCCTAGACCAAGGCGCTATGT 398  
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134 AGAGCCTCTGAAATGATTGGGCTATGGGCGCCGAGCAGTTTCAGTGAATGAAGTGAACC 193  
|||  
397 ACGCCTCTGAAATGATTGGGCTATGGGCGCCGAGCAGTTTCAGTGAATGAAGTGAACC 338  
|||  
194 AGCAACACCTGAAAGAGGGGAACCCAGCAACTCAAGTCAAGATCCTGAGCTCTGAGTGA 253  
|||  
337 AGCAACACCTGAAAGAGGGGAACCCAGCAACTCAAGTCAAGATCCTGAGCTCTGAGTGA 278  
|||  
254 GGGAGAGGATGAGGAGGAGATCTCAGGTCAAGGCGCGAAGCCTGAAGCTCATAGCCAGGA 313  
|||  
277 GGGAGAGGATGAGGAGGAGATCTCAGGTCAAGGCGCGAAGCCTGAAGCTCATAGCCAGGA 218  
|||  
314 ACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGCGAGAGTGA 373  
|||  
217 ACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGCGAGAGTGA 158  
|||  
374 CCGCCCAATCCAGAGGAGTGAAGACGCTGAAGAGGTGAAGCAATCACAGTGTGA 433  
|||  
157 CCGCCCAATCCAGAGGAGTGAAGACGCTGAAGAGGTGAAGCAATCACAGTGTGA 98  
|||  
434 AAGAGACACGTTGAATGATGACGCTGTCTCTATGTTGGAATTTGTTCAATTAAT 493  
|||  
97 AAGAGAGGACGTTGAATGATGACGCTGTCTCTATGTTGGAATTTGTTCAATTAAT 38  
|||  
494 TCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 530  
|||  
37 TCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 1

RESULT 8  
AI381509/c  
LOCUS  
DEFINITION  
IMAGE:2092597 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;  
mRNA sequence.  
AI381509  
AI381509.1 GI:4194290  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 447)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 497 Std Error: 0.00  
Seq primer: -40UP from Gibco.  
Location/Qualifiers  
1..447  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2092597"  
/lab\_host="DH10B"  
/clone\_lib="Soares NFL T GBC S1"  
/note="Organ: pooled; Vector: p7T3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NbHL19W, testis NHT, and B-cell  
NCI-CCAP\_GCB1) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo. "

ORIGIN  
Query Match 78.9%; Score 424.6; DB 9; Length 447;  
Best Local Similarity 98.4%; Pred. NO. 2.8e-85;  
Matches 440; Conservative 0; Mismatches 4; Indels 3; Gaps 1;  
QY 88 GTTGGCGAGGAGATCGACC---TATCGCCTAGACCAAGAGCCTACGTAGAGCTCTCTG 144  
|||  
Db 447 GTTGGCGAGGAGATCGACCCTATTATGGCCTAGACCAAGGCGCTATGTACAGCTCTCTG 388  
|||  
QY 145 AAATGATTGGGCTATGCGGCGCCGAGCAGTTTCAGTGAATGGAACCAAGCAACACCTG 204  
|||  
Db 387 AAATGATTGGGCTATGCGGCGCCGAGCAGTTTCAGTGAATGGAACCAAGCAACACCTG 328  
|||  
QY 205 AAGAAGGGGAACAGCAACTCAACGTCAGGATCTCTGAGTGTGAGGAGGAGAGGATG 264  
|||  
Db 327 AAGAAGGGGAACAGCAACTCAACGTCAGGATCTCTGAGTGTGAGGAGGAGAGGATG 269  
|||  
QY 265 AGGAGCATCTGAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGG 324  
|||  
Db 267 AGGAGCATCTGAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGG 208  
|||  
QY 325 CACAGACTGGTGTGAGTGTGAAGATGGTCTCTGATGGCGAGGAGATGGAACCCGCAATC 384  
|||  
Db 207 CACAGACTGGTGTGAGTGTGAAGATGGTCTCTGATGGCGAGGAGATGGAACCCGCAATC 148  
|||  
QY 385 CAGAGGAGGTGAAGAACGCTGAGAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGG 444  
|||  
Db 147 CAGAGGAGGTGAAGAACGCTGAGAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGG 88  
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QY 445 GTTCAATGATGAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGG 504  
|||  
Db 87 GTTCAATGATGAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGG 28  
|||  
QY 505 AGCTTTACAGCCTTCTGCAAGAAAAA 531  
|||  
Db 27 AGCTTTACAGCCTTCTGCAAGAAAAA 1

RESULT 9  
AA738037/c  
LOCUS  
DEFINITION  
IMAGE:1511.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3'  
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ; mRNA sequence.  
AA738037  
AA738037.1 GI:2768794  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 464)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 511 Std Error: 0.00  
Seq primer: -40m3 fwd. ET from Amersham  
High quality sequence stop: 435.

## FEATURES

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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:1256204"  
 /issue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP GC3"  
 /note="Vector: pTVT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - cligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTVT3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 78.9%; Score 424.4; DB 9; Length 464;  
 Best Local Similarity 96.9%; Pred. No. 3.1e-85;  
 Matches 444; Conservative 0; Mismatches 11; Indels 3; Gaps 1;  
 QY 84 ATGAGTTGGCGAGGAAGATCGACCTTTATTCGCTAGTCCAGACGCTATGTCAGCCT 140  
 Db |||||||  
 QY 464 ATGAGTTGGCGAGGAAGATCGACCTTTATTCGCTAGTCCAGACGCTATGTCAGCCT 405  
 Db |||||||  
 QY 141 COTGAATGATTGGGCTTATCGGCGCCGAGCAGTTCAGTGATGAAGTGAACCAACA 200  
 Db |||||||  
 QY 404 COTGAATGATTGGGCTTATCGGCGCCGAGCAGTTCAGTGATGAAGTGAACCAACA 345  
 Db |||||||  
 QY 201 COTGAAGAGGGAACCAAGCACTCAACGTCAGGATCTCGAGCTGCTCAGGAGGAG 260  
 Db |||||||  
 QY 344 COTGAAGAGGGAACCAAGCACTCAACGTCAGGATCTCGAGCTGCTCAGGAGGAG 285  
 Db |||||||  
 QY 261 GATGAGGAGCATTCGAGGTCAAGGCGCAAGCTGAAGCTCATAGCCAGAAACAGGGT 320  
 Db |||||||  
 QY 284 GATGAGGAGCATTCGAGGTCAAGGCGCAAGCTGAAGCTCATAGCCAGAAACAGGGT 225  
 Db |||||||  
 QY 321 CACCCACAGCTGGGTGTCAGTGTCAAGATGCTCTGATGGCAGGATGACCCGCCA 380  
 Db |||||||  
 QY 224 CACCCACAGCTGGGTGTCAGTGTCAAGATGCTCTGATGGCAGGATGACCCGCCA 165  
 Db |||||||  
 QY 381 AATCCAGAGGAGTGAACACCGCTCAAGAAGTGAAGCAATCACTGTTTAAAGAG 440  
 Db |||||||  
 QY 164 AATCCAGAGGAGTGAACACCGCTCAAGAAGTGAAGCAATCACTGTTTAAAGAG 105  
 Db |||||||  
 QY 441 ACAGTTGAATGATGCGAGGTGCTCTATGTTGAAATTTGTTCAATTAATTTCTCCA 500  
 Db |||||||  
 QY 104 GCAGCTTGAATGATGCGAGGTGCTCTATGTTGAAATTTGTTCAATTAATTTCTCCA 45  
 Db |||||||  
 QY 501 ATAAGCTTTACAGCTTCTCAGAGAAAAA 538  
 Db |||||||  
 QY 44 ATAAGCTTTACAGCTTCTCAGAGAAAAA 7  
 Db |||||||

## RESULT 10

CB115693  
 LOCUS X-EST0159805 L8SCK0 Homo sapiens cDNA clone L8SCK0-8-B09 5', mRNA  
 DEFINITION K-EST0159805 L8SCK0 Homo sapiens cDNA clone L8SCK0-8-B09 5', mRNA  
 sequence.  
 CB115693  
 VERSION CB115693.1 GI:27941500  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 505)  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001

## JOURNAL

COMMENT Unpublished (2002)  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 8 row: B column: 09  
 High quality sequence stop: 505.

## FEATURES

source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="L8SCK0-8-B09"  
 /sex="M"  
 /cell\_line="SCK"  
 /lab\_host="Trop10F"  
 /clone\_lib="L8SCK0"  
 /note="Organ: Liver; Vector: pTVT3-Pac; Site 1: EcoRI; Site 2: NotI; The library was constructed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

## ORIGIN

Query Match 77.2%; Score 415.2; DB 14; Length 505;  
 Best Local Similarity 96.5%; Pred. No. 3.7e-83;  
 Matches 436; Conservative 0; Mismatches 13; Indels 3; Gaps 1;  
 QY 32 GTTCCTGCCGTCGCGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGTTG 91  
 Db |||||||  
 QY 19 GGTCTGCGGTCGCGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGTTG 78  
 Db |||||||  
 QY 92 GCGAGGAGATCGACC---TATCGGCTAGACCAAGACGCTACGTAGAGCTCTCTGAAAT 148  
 Db |||||||  
 QY 79 GCGAGGAGATCGACCTATTATTGGCTTAGACCAAGGCGCTATGTACAGCTCTCTGAAAT 138  
 Db |||||||  
 QY 149 GATTGGGCTATGCGCCGAGCAGTTCAGTGATGAGTGAAGTGAACCAAGCAACCTGAGA 208  
 Db |||||||  
 QY 139 GATTGGGCTATGCGCCGAGCAGTTCAGTGATGAGTGAAGTGAACCAAGCAACCTGAGA 198  
 Db |||||||  
 QY 209 AGGGGAACCAAGCAACTCAACGTCAGGATCTCTGAGCTGCTCAGGAGGAGAGTGAAGG 268  
 Db |||||||  
 QY 199 AGGGGAACCAAGCAACTCAACGTCAGGATCTCTGAGCTGCTCAGGAGGAGAGTGAAGG 258  
 Db |||||||  
 QY 269 AGCATCTGAGGTCAAGGCGCGAAGCCTGAAGCTCTATAGCCAGGAAACAGGTCACCCACA 328  
 Db |||||||  
 QY 259 AGCATCTGAGGTCAAGGCGCGAAGCCTGAAGCTCTATAGCCAGGAAACAGGTCACCCACA 318  
 Db |||||||  
 QY 329 GACTGGGTGTGAGTGTCAAGATGCTCTGATGGCAGGAGATGACCCGCAATCCAGA 388  
 Db |||||||  
 QY 319 GACTGGGTGTGAGTGTCAAGATGCTCTGATGGCAGGAGATGACCCGCAATCCAGA 378  
 Db |||||||  
 QY 389 GGAGGTGAAAACCGCTCAAGHAGGTGAAAAGCAATCACTGTTTAAAGAGACACCTTG 448  
 Db |||||||  
 QY 379 GGAGGTGAAAACCGCTCAAGHAGGTGAAAAGCAATCACTGTTTAAAGAGACATCTG 438  
 Db |||||||  
 QY 449 AAATGATGCGAGGTGCTCTCTATGTTGAAAT 480  
 Db |||||||  
 QY 439 AAATGTTGCGAGGTGCTCTCTATGTTGAAACT 470  
 Db |||||||

## RESULT 11

AW016546/c  
 LOCUS AW016546 418 bp mRNA linear EST 10-SEP-1999  
 DEFINITION UI-H-B10p-abg-g-06-0-UI.s1 NCI CGAP\_Sub2 Homo sapiens cDNA clone  
 IMAGE:2711986 3', mRNA sequence.  
 ACCESSION AW016546  
 VERSION AW016546.1 GI:5865303  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 418)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 The sequence contained an oligo-dT track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:  
 NCI-CGAP clone distribution information can be found through the  
 I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: M13 Forward  
 POLYA=Yes.

FEATURES  
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 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2711986"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI\_CGAP\_Sub2"  
 /notes="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The  
 NCI\_CGAP Sub2 library is a subtracted library derived from  
 B1. BI constitutes a mixture of 21 normalized or  
 subtracted NCI CGAP libraries: NCI\_CGAP\_C04,  
 NCI\_CGAP\_Pr22, NCI\_CGAP\_Pr28, NCI\_CGAP\_C010,  
 NCI\_CGAP\_C016, NCI\_CGAP\_Kid5, NCI\_CGAP\_Kid12,  
 NCI\_CGAP\_Kid3, NCI\_CGAP\_Kid11, NCI\_CGAP\_Lym2,  
 NCI\_CGAP\_Br2, NCI\_CGAP\_C08, NCI\_CGAP\_C111, NCI\_CGAP\_Le12,  
 NCI\_CGAP\_Brn23, NCI\_CGAP\_Lu5, NCI\_CGAP\_Lu24,  
 NCI\_CGAP\_Brn25, NCI\_CGAP\_GC4, NCI\_CGAP\_GC6, NCI\_CGAP\_Brn25.  
 These 21 libraries were pooled and a single-stranded DNA  
 preparation of the resulting mixture was used as a tracer  
 in a subtractive hybridization with a driver whose  
 composition is detailed below: NCI\_CGAP\_Kid3 pool 1 LLAM  
 3334-3337, 3682-3683, 3798-3803 (IMAGE Clones)  
 1323276-1323911, 1456008-1456775, 1500552-1502855)  
 NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778  
 (IMAGE Clones 1323912-1325831, 1471368-1472903,  
 1492104-1493255) NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582,  
 3851-3854 (IMAGE Clones 1414920-1417991,  
 1520904-1522439) NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167,  
 3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631,  
 1469064-1470983, 1475592-1476743) NCI\_CGAP\_Pr22 pool 1  
 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones  
 985608-986759, 1101192-1101959, 1217928-1220615)  
 NCI\_CGAP\_C010 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE  
 Clones 1057416-1061255, 1144584-1145351) The resulting  
 subtracted library contained 4 million recombinants.  
 Subtraction was performed as previously described  
 [Bonaldo, Lennon & Soares (1996): Normalization and  
 Subtraction: Two Approaches To Facilitate Gene Discovery.  
 Genome Research 6, 791-806.  
 TAG\_TISSUE=germ cell  
 TAG\_LIB=NCI\_CGAP\_GC4  
 TAG\_SEQ=AAATC

ORIGIN  
 Query Match 76.9%; Score 413.8; DB 9; Length 418;  
 Best Local Similarity 99.5%; Pred. No. 7.5e-83;  
 Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 122 AAGACGCTACGTAGAGCTCTCTGAATGATGGCGCTATCGGCCCGAGCGAGTTCAGTGA 181  
 Db  
 418 AAGACGCTACGTAGAGCTCTCTGAATGATGGCGCTATCGGCCCGAGCGAGTTCAGTGA 359

QY 182 TGAAGTGGAAACAGCAACACCTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCCTGC 241  
 Db 358 TGAAGTGGAAACAGCAACACCTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCCTGC 299  
 QY 242 AGCTCTCAGGAGGAGAGGATGAGGGAGCATCTCAGGTCAAGGCCGAGCCTGAAGC 301  
 Db 298 AGCTCTCAGGAGGAGAGGATGAGGGAGCATCTCAGGTCAAGGCCGAGCCTGAAGC 239  
 QY 302 TCATAGCCAGGAACAGGCTCACCACAGACTGGGTGTGAGTGTGAAGATGGTCTCATGG 361  
 Db 238 TCATAGCCAGGAACAGGCTCACCACAGACTGGGTGTGAGTGTGAAGATGGTCTCATGG 179  
 QY 362 GCAGAGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCCTGAAGAGGTGAAAAGCA 421  
 Db 178 GCAGAGAGTGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCCTGAAGAGGTGAAAAGCA 119  
 QY 422 ATCAGAGTGTAAAAGAGACACGTTGAAATGATGAGCGTCTCTCTATGTGGAAATTT 481  
 Db 118 ATCAGAGTGTAAAAGAGAGCGACGTTGAAATGATGAGCGTCTCTCTATGTGGAAATTT 59  
 QY 482 GTTCATTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 538  
 Db 58 GTTCATTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 2

RESULT 12  
 BG120336 480 bp mRNA linear EST 30-JAN-2001  
 602353732f1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:4451958 5',  
 LOCUS mRNA sequence.  
 BG120336  
 ACCESSION BG120336.1 GI:12613845  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 480)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM10239 row: p column: 07  
 High quality sequence stop: 480.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:4451958"  
 /tissue\_type="adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_90"  
 /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.7 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 76.8%; Score 413.4; DB 12; Length 480;  
 Best Local Similarity 97.4%; Pred. No. 9.3e-83;  
 Matches 420; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 108 TATCGGCTAGACCAAGACGCTAGCTAGAGCTCTGAAATGATTGGCCCTATCGGCC 167  
 Db |||||  
 QY 15 TATTGGCTAGACCAAGCGCTATGTATACAGCTCTGAGTGATTTGGCCCTATCGGCC 74  
 Db |||||  
 QY 168 GAGCAGTTCAAGTGAAGTGGACCAACAGCAACACCTGAAGAAGGGAACCAAGCAACTCAA 227  
 Db |||||  
 QY 75 GAGCAGTTCAAGTGAAGTGGACCAACAGCAACACCTGAAGAAGGGAACCAAGCAACTCAA 134  
 Db |||||  
 QY 228 CTTGAGGATCTGAGCTGCTCAGAGGAGAGAGATGAGGAGATCTGAGGTCAAGGG 287  
 Db |||||  
 QY 135 GTCAGATCTGAGCTGCTCAGAGGAGAGAGATGAGGAGATCTGAGGTCAAGGG 194  
 Db |||||  
 QY 288 CCGAAGCTCAAGCTCATAGCCAGCAACAGGTCACCCACAGACTGGGTGTGAGTGTGAA 347  
 Db |||||  
 QY 195 CCGAAGCTCAAGCTCATAGCCAGCAACAGGTCACCCACAGACTGGGTGTGAGTGTGAA 254  
 Db |||||  
 QY 348 GATGGTCTGATGGGAGGAGATGGACCGCAATCCAGAGGAGTGAAGCGCTGAA 407  
 Db |||||  
 QY 255 GATGGTCTGATGGGAGGAGATGGACCGCAATCCAGAGGAGTGAAGCGCTGAA 314  
 Db |||||  
 QY 408 GAAGGTCAAAAGCAATCACAGTGTAAAGAAGACAGCTTGAATGATGAGGTGCTCC 467  
 Db |||||  
 QY 315 GAAGGTCAAAAGCAATCACAGTGTAAAGAAGACAGCTTGAATGATGAGGTGCTCC 374  
 Db |||||  
 QY 468 TATGTTGGAAATTTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAGA 527  
 Db |||||  
 QY 375 TATGTTGGAAATTTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAGA 434  
 Db |||||  
 QY 528 AAAAAAAAAA 538  
 Db |||||  
 QY 435 AAAAAAAAAA 445

RESULT 13  
 AA868226/c  
 LOCUS  
 DEFINITION  
 3' similar to SW:GGE2\_HUMAN Q13066 GAGE-2 PROTEIN. [1] ;, mRNA  
 sequence.  
 ACCESSION  
 AA868226  
 VERSION  
 AA868226.1 GI:2963671  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 426)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Possible reversed clone: similarity on wrong strand  
 Seq primer: -40m3 fwd. ET from Amersham  
 High quality sequence stop: 363.

## FEATURES

Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1409245"  
 /sex="male"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares\_testis\_NHT"

## ORIGIN

Query Match 76.7%; Score 412.8; DB 9; Length 426;  
 Best Local Similarity 97.9%; Pred. No. 1.3e-82;  
 Matches 417; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 102 TCGACCTATCGGCTTAGACCAAGCCTACGTAGAGCTCTCTGAAATGATTTGGCCCTATG 161  
 Db |||||  
 QY 426 TCGACCTATCGGCTTAGACCAAGCCTACGTAGAGCTCTCTGAAATGATTTGGCCCTATG 367  
 Db |||||  
 QY 162 CGGCCCGAGCAGTTCAGTGAAGTGGACCAAGCAACCTCTGAAGAAGGGAACCAAGCA 221  
 Db |||||  
 QY 366 CGGCCCGAGCAGTTCAGTGAAGTGGACCAAGCAACCTCTGAAGAAGGGAACCAAGCA 307  
 Db |||||  
 QY 222 ACTCAACGTCAGGATCTCGCAGCTCTCAGGAGGAGAGATGAGGAGCATCTGCAGGT 281  
 Db |||||  
 QY 306 ACTCAACGTCAGGATCTCGCAGCTCTCAGGAGGAGAGATGAGGAGCATCTGCAGGT 247  
 Db |||||  
 QY 282 CAGGGCCCAAGCCTCAAGCTCATAGCCAGGAACAGGGTCACCAAGCTGGGTGTGAG 341  
 Db |||||  
 QY 246 CAGGGCCCAAGCCTCAAGCTCATAGCCAGGAACAGGGTCACCAAGCTGGGTGTGAG 187  
 Db |||||  
 QY 342 TGTGAAGATGGTCTCTGATGGCAGGAGATGGACCGCCAAATCCAGAGGAGTGAAGCG 401  
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 QY 186 TGTGAAGATGGTCTCTGATGGCAGGAGATGGACCGCCAAATCCAGAGGAGTGAAGCG 127  
 Db |||||  
 QY 402 CTTGAAGAAGGTGAAGAAGCAATCACAGTGTAAAAGAGACACGTTGAAATGATGAGGC 461  
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 QY 462 TGTCTCTATGTTGGAATTTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCTTCTG 521  
 Db |||||  
 QY 66 TGTCTCTATGTTGGAATTTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCTTCTT 7  
 Db |||||  
 QY 522 CAAAGA 527  
 Db |||||  
 QY 6 CAAAAA 1

## RESULT 14

AA760996/c  
 LOCUS  
 DEFINITION  
 450 bp mRNA linear EST 26-JAN-1998  
 similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.  
 ACCESSION  
 AA760996  
 VERSION  
 AA760996.1 GI:2809926  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 450)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was prepared from mRNA obtained from Clontech  
 Laboratories, Inc., and primed with a Not I - oligo(dT)  
 primer [5].  
 TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'.  
 Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT7T3 vector. Library  
 went through one round of normalization to Cots, and was  
 constructed by Bento Soares and M. Fatima Bonaldo. "

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -40m13 fwd. RT from Amersham  
High quality sequence stop: 331.

FEATURES

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/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP GC4"  
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polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified p7T3  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 76.4%; Score 410.8; DB 9; Length 450;  
Best Local Similarity 97.3%; Pred. No. 3.6e-82; Indels 4; Gaps 2;  
Matches 439; Conservative 0; Mismatches 8;  
QY 84 ATGAGTTGGCGAGGAAGATCGACC---TATCGGCTAGACCAAGACGCTAGTAGAGCT 140  
Db 450 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCT 391  
QY 141 CCTGAATGATTTGGCCCTATGCGGCCGAGCAGTTTCAGTGATGAAGTGAACCAACACACA 200  
Db 390 CCTGAATGANTGTGCCTATGCGGCCGAGCAGTTTCAGTGATGAAGTGAACCAACACACA 331  
QY 201 CCTGAAGAGGGAACCAAGCACTCAAGTCAGGATCTGAGCTGCTCAGGAGGAGAG 260  
Db 330 CCTGAAGAGGGAACCAAGCACTCAAGTCAGGATCTGAGCTGCTCAGGAGGAGAG 271  
QY 261 GATGAGGAGCAGTCATGCGAGGTCAAGGCGCGAAGCTCAAGCTCATPAGCCAGGAACAGGCT 320  
Db 270 GATGAGGAGCAGTCATGCGAGGTCAAGGCGCGAAGCTCAAGCTCATPAGCCAGGAACAGGCT 211  
QY 321 CACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGGACCCGCCA 380  
Db 210 CACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGGACCCGCCA 151  
QY 381 ATCCAGAGGAGTGAACACGCTGAAGAGGTGAAGCAATCAAGTGTAAAGAGAG 440  
Db 150 ATCCAGAGGAGTGAACACGCTGAAGAGGTGAAGCAATCAAGTGTAAAGAGAG 91  
QY 441 ACACGTTGAATGATGCGAGGCTGCTCCTATGTTGAAATTTGTTCAATTAATTTCTCCCA 500  
Db 90 ACACGTTGAATGATGCGAGGCTGCTCCTATGTTGAAATTTGTTCAATTAATTTCTCCCA 31  
QY 501 ATAAAGCTTACAGCTTCTGCAAGAAAAA 531  
Db 30 ATAAAG-ATTACAGCTTCTGCAAAAAAAA 1

RESULT 15

Al187350/c  
LOCUS  
DEFINITION  
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sequence.  
ACCESSION  
Al187350  
VERSION  
Al187350.1 GI:3737988  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 455)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert length: 504 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 391.

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/sex="male"  
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/clone\_lib="Soares testis NHT"  
/note="vector: p7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5].  
TGTACCAATCTGAAGTGGGCGCGCCCAATTTTTTTTTTTT 3'.

Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

IGTACCAATCTGAAGTGGGCGCGCCCAATTTTTTTTTTTT 3'.

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(Pharmacia), digested with Not I and cloned into the Not I  
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and Eco RI sites of the modified p7T3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

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(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. Library  
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constructed by Bento Soares and M. Fatima Bonaldo."

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(Pharmacia), digested with Not I and cloned into the Not I  
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and Eco RI sites of the modified p7T3 vector. Library  
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and Eco RI sites of the modified p7T3 vector. Library  
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(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. Library  
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and Eco RI sites of the modified p7T3 vector. Library  
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and Eco RI sites of the modified p7T3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

QY 502 TAAAGCTTTACAGCCTTCTGCAAGAAAAA 537  
DB 36 TAAAGCTTTCCAGCCTTCTGCAAAAAA 1

Search completed: August 8, 2004, 12:43:19  
Job time : 2817 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2004, 09:50:03 ; Search time 372 Seconds

(without alignments)  
6143.899 Million cell updates/sec

Title: US-09-782-745-14

Perfect score: 538

Sequence: 1 ACGCCAGGAGCTGTGAGGC.....CTGCAAGAGAAAAA 538

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 5017792

Minimum DB seq length: 0

Maximum DB seq length: 538

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002s:\*
- 7: geneseqn2003as:\*
- 8: geneseqn2003bs:\*
- 9: geneseqn2003cs:\*
- 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	538	100.0	538	2 AAX90519	Aax90519 GAGE-2 tu
2	530	98.5	530	7 ABZ20463	Abz20463 GAGE-2 fu
3	525.4	97.7	528	7 ADAL5801	Adal5801 Human GAG
4	504.8	93.8	532	2 AAX90522	Aax90522 GAGE-5 tu
5	501.4	93.2	528	6 ABZ166323	Abz166323 Lung canc
6	498.8	92.7	527	7 ACC51027	Acc51027 Human bla
7	498.8	92.7	527	7 ABX76236	Abx76236 Lung canc
8	496.8	92.3	532	2 AAV18720	Aav18720 cDNA enco
9	493	91.6	535	2 AAV18717	Aav18717 cDNA enco
10	488	90.7	526	7 ADAL5802	Adal5802 Human GAG
11	357.8	66.5	430	3 AAC02129	Aac02129 Human sec
12	301.4	56.0	530	4 AAS60104	Aas60104 Human can
13	299.2	55.6	365	4 AAS60496	Aas60496 Human can
14	241.4	44.9	259	7 ABZ19791	Abz19791 Group III
15	225	41.8	225	7 ABZ19533	Abz19533 Group III
16	223.6	41.6	257	7 ABZ19955	Abz19955 Group III
17	223.6	41.6	264	7 ABZ19755	Abz19755 Group III
18	222	41.3	277	7 ABZ19551	Abz19551 Group III
19	216.6	40.3	520	7 ABT15737	Abt15737 Human can
20	209	38.8	509	7 ABX77605	Abx77605 Different
21	209	38.8	509	8 ACB42232	AcB42232 Human GAG
22	209	38.8	509	9 ADC24646	Adc24646 Human cDN
23	206.6	38.4	229	7 ABZ20497	Abz20497 TPS1 subt

C	24	203	37.7	227	7	ABZ20480	Abz20480 TPS1 subt
c	25	202	37.5	229	7	ABZ18686	Abz18686 Group III
	26	201	37.4	219	7	ABZ19538	Abz19538 Group III
	27	194	36.1	532	4	AAI60530	Aai60530 Human pol
	28	172.4	32.0	503	5	AAS69484	Aas69484 DNA enco
	29	153	28.4	528	7	ABT15728	Abt15728 Human can
	30	130.4	24.2	475	4	ADL14981	Adl14981 Human NOV
	31	125.4	23.3	538	7	ABT15736	Abt15736 Human can
	32	108	20.1	399	5	AAF68151	Aaf68151 Human lun
	33	108	20.1	399	6	ABK38062	Abk38062 cDNA enco
	34	108	20.1	399	7	ACA10391	Aca10391 Human lun
	35	108	20.1	399	7	ABX99342	Abx99342 Lung canc
	36	108	20.1	399	10	ABE72125	Abe72125 Human lun
	37	103.6	19.3	505	6	AAD24228	Aad24228 Human dif
	38	103.4	19.2	463	6	ABA92217	Aba92217 Melanoma
	39	101.6	18.9	515	4	AAH93807	Aah93807 Human pro
	40	101.6	18.9	515	4	AAAG63900	Aas63900 Human pro
	41	101.6	18.9	515	4	AAH02872	Aah02872 Prostate
	42	101.6	18.9	515	4	AAH85121	Aah85121 Human pro
	43	101.6	18.9	515	5	ACA59708	Aca59708 Prostate
	44	101.6	18.9	515	6	ABL95271	Ab195271 Human P10
	45	101.6	18.9	515	7	ACC95435	Acc95435 Prostate

## ALIGNMENTS

RESULT 1  
AAX90519  
ID AAX90519 standard; cDNA; 538 BP.  
XX  
AC AAX90519;  
XX  
DT 30-SEP-1999 (first entry)  
XX  
DE GAGE-2 tumour rejection antigen clone nucleotide sequence.  
XX  
KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
KW GAGE; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9937665-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 12-JAN-1999; 99WO-US000775.  
XX  
PR 23-JAN-1998; 98US-00012818.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;  
XX  
DR WPI; 1999-469111/39.  
XX  
PT New isolated peptides which bind to HLA-A29 molecules, which are tumor  
PT rejection antigens used for detection and therapy of pathological  
PT conditions, e.g. cancer.  
XX  
PS Example 13; Fig 4; 62pp; English.  
XX  
CC The present invention describes peptides which bind to human leukocyte  
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into  
CC tumour rejection antigens. They can be used for detecting cytolytic T  
CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-  
CC typing assays. Complexes of HLA-29 molecules and the peptides can be used  
CC for stimulating CTLs in vivo. The present sequence represents a GAGE  
CC tumour rejection antigen clone, from an example from the present  
XX invention  
XX  
SQ Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;





1	AGCTGTGAGGCAGTCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTACTAGATT	60
70	CATCTGTGTGAATAATGATGATTGGCGAGGAAGATCGACC--TATCGGCTTAGCAACGAC	126
61	CATCTGTGTGAATATGATGATTGGCGAGGAAGATGACCTNTATTATTTGGCTTAGCAAGGC	120
127	GCTACGTAGAGCCCTCCTGAATGATTTGGGCCCTATTCGGGCCCGAGCAGTTTCAGTGTGAAG	186
121	GCTATGTPACAGCCTCCTGAAGTGTATGGSCCTATTCGGGCCCGAGCAGTTTCAGTGTGAAG	180
187	TGGAACACAGCAACCTGGAAGAGGGGAAACAGCGAACTCAAGTCAGGATCCTCGAGCTG	246
181	TGGAACACAGCAACCACTGAAGAAGGGGAACCAAGCAACTCAACGTGAGGATCCTCGAGCTG	240
247	CTCAGGAGGGAGAGATCAGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCAT	306
241	CTCAGGAGGGAGAGATGAGGAGGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATA	300
307	GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGCGAGG	366
301	GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGCGAGG	360
367	AGATGGAACCCGCCAAATCCAGAGAGGTGAAAACGCCCTGAAGAAAGTGAAGAAGCAATCAC	426
361	AGATGGAACCCGCCAAATCCAGAGAGGTGAAAACGCCCTGAAGAAAGTGAAGAAGCAATCAC	420
427	AGTGTTTAAAGAAGACAGTTGAAATGATGCAAGGTGCTCCTATGTGTGAAATTTGTTTCA	486
421	AGTGTTTAAAGAAGACAGTTGAAATGATGCAAGGTGCTCCTATGTGTGAAATTTGTTTCA	480
487	TTAAATTTCTCCCAATAAGCTTTACGCCCTTCTGCAAGAAAAA	538
481	TTAAATTTCTCCCAATAAGCTTTACGCCCTTCTGCAAGAAAAA	532

RESE, T 5

XX	ABL66323	standard; DNA; 528 BP.
XX	AC	ABL66323;
XX	AC	ABL66323;
DT	15-MAY-2002	(first entry)
XX	XX	Lung cancer related gene sequence SEQ ID NO:4660.
DE	XX	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX	XX	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	XX	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW	XX	gene; ds.
KW	XX	Homo sapiens.
OS	XX	WO2001194629-A2.
XX	XX	13-DEC-2001.
PD	XX	30-MAY-2001; 2001WO-US010838.
XX	XX	05-JUN-2000; 2000US-0209473P.
PR	XX	05-JUN-2000; 2000US-0209531P.
PR	XX	18-SEP-2000; 2000US-0233133P.
PR	XX	18-SEP-2000; 2000US-0233617P.
PR	XX	20-SEP-2000; 2000US-0234009P.
PR	XX	20-SEP-2000; 2000US-0234034P.
PR	XX	20-SEP-2000; 2000US-0234052P.
PR	XX	22-SEP-2000; 2000US-0234509P.
PR	XX	22-SEP-2000; 2000US-0234567P.
PR	XX	25-SEP-2000; 2000US-0234923P.
PR	XX	25-SEP-2000; 2000US-0234924P.
PR	XX	25-SEP-2000; 2000US-0235077P.
PR	XX	25-SEP-2000; 2000US-0235082P.
PR	XX	25-SEP-2000; 2000US-02351134P.

RESULT 5  
 ABL66323  
 ID ABL66323 standard; DNA; 528 BP.  
 XX  
 XX AC ABL66323;  
 XX AC ABL66323;  
 DT 15-MAY-2002 (first entry)  
 XX  
 DE XX Lung cancer related gene sequence SEQ ID NO:4660.  
 XX  
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
 KW gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2001194629-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 XX 30-MAY-2001; 2001WO-US010838.  
 XX  
 XX 05-JUN-2000; 2000US-0209473P.  
 PR 05-JUN-2000; 2000US-0209531P.  
 PR 18-SEP-2000; 2000US-0233133P.  
 PR 18-SEP-2000; 2000US-0233617P.  
 PR 20-SEP-2000; 2000US-0234009P.  
 PR 20-SEP-2000; 2000US-0234034P.  
 PR 20-SEP-2000; 2000US-0234052P.  
 PR 22-SEP-2000; 2000US-0234509P.  
 PR 22-SEP-2000; 2000US-0234567P.  
 PR 25-SEP-2000; 2000US-0234923P.  
 PR 25-SEP-2000; 2000US-0234924P.  
 PR 25-SEP-2000; 2000US-0235077P.  
 PR 25-SEP-2000; 2000US-0235082P.  
 PR 25-SEP-2000; 2000US-02351134P.

Claim 1; SEQ ID NO 4660; 44pp; English.  
 The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour  
 Sequence 528 BP; 147 A; 114 C; 156 G; 111 T; 0 U; 0 Other;  
 Query March 93.2%; Score 501.4; DB 6; Length 528;  
 Best Local Similarity 98.3%; Pred. No. 2.6e-135;  
 Matches 518; Conservative 0; Mismatches 6; Indels 3; Gaps 1  
 QY 2 CGCCAGGAGCTGTGAGGCAGTCTGTGTGTTTCTCTCGCGTCTTTTCTCTA 61  
 Db 1 CGCCAGGAGCTGTGAGGCAGTCTGTGTGTTTCTCTCGCGTCTTTTCTCTA 60  
 QY 62 CTGAGATTCATCTGTGTGAATATGAGTTGCCAGGAGATGCACC---TATCGGCTAG 118  
 Db 61 CTGAGATTCATCTGTGTGAATATGAGTTGCCAGGAGATGCACCTATTATTGGGCTAG 120





CC of melanoma using cytolytic T cell clone proliferation methodologies.  
 CC Other uses for the processed peptides, include HLA-typing assays for,  
 CC e.g. skin graft or organ transplants

XX SQ Sequence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 U; 0 Other;

Query Match 92.3%; Score 496.8; DB 2; Length 532;  
 Best Local Similarity 97.2%; Pred. No. 5.6e-134;  
 Matches 517; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 10 AGCTGTGAGGACGTCTGTGTGGTTCCTGCGGTCGGACTCTTTTCCCTCTACTGAGATT 69  
 Db 1 AGCTGTGAGGACGTCTGTGTGGTTCCTGCGGTCGGACTCTTTTCCCTCTACTGAGATT 60

QY 70 CATCTGTGTGAATATGAGTTCGCGAGGAAGATCGACC---TATCGGCTAGACCAAGAC 126  
 Db 61 CATCTGTGTGAATATGAGTTCGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC 120

QY 127 GCTACTGAGGACCTCTCTGAAATGATTTGGCCCTATGCGGCCGAGCAGTTCAGTGTGAAG 186  
 Db 121 GGTATGTACAGCTCTCTGAAAGTGAATTTGGCCCTATGCGGCCGAGCAGTTCAGTGTGAAG 180

QY 187 TGGAAACCAACAAACACTGTAAGAAGGGGAACCAAGCACTCAAGCTCAGGATCCTGCACTG 246  
 Db 181 TGGAAACCAAGCTCTCTGAAAGGGGAACCAAGCACTCAAGCTCAGGATCCTGCACTG 240

QY 247 CTCAGAGGAGAGATGAGGAGCATCTGCAAGTCAAGGGCGGAAGCTGAGTGTGATA 306  
 Db 241 CTCAGAGGAGAGATGAGGAGCATCTGCAAGTCAAGGGCGGAAGCTGAGTGTGATA 300

QY 307 GCCAGGAACAGAGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGG 366  
 Db 301 GCCAGGAACAGAGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGG 360

QY 367 AGATGACCCGCCAAATCCAGAGGAGGTGAATAACCGCTGAAGAGGTGAAGAGCAATCAC 426  
 Db 361 AGATGACCCGCCAAATCCAGAGGAGGTGAATAACCGCTGAAGAGGTGAAGAGCAATCAC 420

QY 427 AGTGTAAAGAGACACCTTGAATATGATGCAAGGCTGCTCCTATGTGTAATTTGTTC 486  
 Db 421 AGTGTAAAGAGACACCTTGAATATGATGCAAGGCTGCTCCTATGTGTAATTTGTTC 480

QY 487 TTAAATTTCTCCCAATAAAGCTTTACAGCTTCTGCAAGAGAAAAA 538  
 Db 481 TTAAATTTCTCCCAATAAAGCTTTACAGCTTCTGCAAGAGAAAAA 532

RESULT 9  
 AAV18717  
 ID AAV18717 standard; cDNA; 535 BP.  
 XX AC AAV18717;

XX 30-JUL-1998 (first entry)  
 XX cDNA encoding GAGE-2 tumour rejection antigen precursor.

XX GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;  
 KW melanoma; antigen; cytolytic T cell clone proliferation;  
 KW HLA-typing assay; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 CDS 81..431  
 FT /\*tag= a  
 FT /transl\_except= (pos:192..194, aa:Ala)  
 FT /transl\_except= (pos:195..197, aa:Thr)

XX WO9749417-A1.  
 XX 31-DEC-1997.

PF 23-JUN-1997; 97WO-US010850.  
 XX 24-JUN-1996; 96US-00669161.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX Debacker O, Van Den Eynde B, Boon-Falleur T;  
 XX WPI; 1998-076905/07.  
 DR P-PSDB; AAW47599.

XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -  
 PT processed by HLA-Cw6 molecules into peptides, useful to diagnose  
 PT melanomas.

XX Example 13; Fig 4; 60pp; English.

XX The present sequence encodes a GAGE-2 tumour rejection antigen  
 CC precursor (TRAP). The protein is expressed in a number of tumours. In  
 CC contrast the only normal tissue which expresses GAGE TRAP protein is  
 CC testis. Several GAGE TRAPs have been identified (see AAV18717-21). The  
 CC major difference between these proteins and GAGE-1 (AAV05540) is the  
 CC absence of a stretch of 143 bases located at position 379 to 521 of the  
 CC GAGE-1 TRAP sequence. The rest of the sequences show mismatches at  
 CC various position, with the exception of GAGE-3 whose 5' end is totally  
 CC different from the other GAGE cDNAs for the first 112 bases. This region  
 CC of GAGE-3 cDNA contains a long repeat and a hairpin structure. The  
 CC antigens can be used to diagnose melanomas, characterised by expression  
 CC of a TRAP or presentation of a tumour rejection antigen. Antigens shed  
 CC into blood or urine can be observed and then used to confirm a diagnosis  
 CC of melanoma using cytolytic T cell clone proliferation methodologies.  
 CC Other uses for the processed peptides, include HLA-typing assays for,  
 CC e.g. skin graft or organ transplants

XX SQ Sequence 535 BP; 158 A; 112 C; 156 G; 109 T; 0 U; 0 Other;

Query Match 91.6%; Score 493; DB 2; Length 535;  
 Best Local Similarity 97.2%; Pred. No. 7.2e-133;  
 Matches 524; Conservative 0; Mismatches 10; Indels 5; Gaps 2;

QY 1 AGCCAGGAGGAGTGTGAGGACGTGTGTGGTTCCTGCGGTCGGACTCTTTTTCCTC- 59  
 Db 1 AGCCAGGAGGAGTGTGAGGACGTGTGTGGTTCCTGCGGTCGGACTCTTTTTCCTC 56

QY 60 TACTGAGATTCATCTGTGTGAATATGAGTGTGGCGAGGAAGATCACTATCGGCTAGA 119  
 Db 57 TACTGAGATTCATCTGTGTGAATATGAGTGTGGCGAGGAAGATCACTATCGGCTAGA 116

QY 120 CCAAGACGCTAGTAGAGCTCTCGAATGATTTGGGCTATGCGGCGGAGAGTTCAGT 179  
 Db 117 CCAAGACGCTAGTAGAGCTCTCGAATGATTTGGGCTATGCGGCGGAGAGTTCAGT 176

QY 180 GATGAAGTGGAAACCAAGCAACCTCGAAGAGGGGAACCAAGCACTCAAGCTCAGGATCCT 239  
 Db 177 GATGAAGTGGAAACCAAGCAACCTCGAAGAGGGGAACCAAGCACTCAAGCTCAGGATCCT 236

QY 240 GCAGTGTCTCAGGAGGAGAGATGAGGAGCAATCTGAGGTCAAGGGCCGAGGCTGAA 299  
 Db 237 GCAGTGTCTCAGGAGGAGAGATGAGGAGCAATCTGAGGTCAAGGGCCGAGGCTGAA 296

QY 300 GCTCATAGCCAGGACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCAT 359  
 Db 297 GCTCATAGCCAGGACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCAT 356

QY 360 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAACCGCCTGAAGAGGTGAAAG 419  
 Db 357 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAACCGCCTGAAGAGGTGAAAG 416

QY 420 CAATCAGTGTAAAGAGAGACAGTGTGAATGATGAGGCTGCTCTATGTTGGAAT 479  
 Db 417 CAATCAGTGTAAAGAGAGACAGTGTGAATGATGAGGCTGCTCTATGTTGGAAT 476

QY 480 TTGTTTCAATAAATTTCTCCCAATAAAGCTTTTACAGCTTTCTGCAAGAGAAAAA 538

```
Db 477 TTGTCATTAAATCTCCCAATAAGCTTTACAGCCTTCTGCAAGAAAAA 535
|||||
RESULT 10
ADA15802
ID ADA15802 standard; cDNA; 526 BP.
XX
XX
AC ADA15802;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human GAGE-7B cDNA.
XX
XX Human; GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL;
XX human leukocyte antigen; HLA; tumour rejection antigen precursor;
XX major histocompatibility complex; MHC; cytolytic T cell proliferation;
XX chromosome Xp11.2-p11.4.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 55..408
XX /*tag= a
XX /product= "Human GAGE-7B"
XX /transl_except= (pos:115..162, aa: GPMRPEOGSDVPSMI)
XX /transl_except= (pos:265..306, aa: HPQTGKEAHSQE)
XX
XX US6509172-B1.
XX
XX 21-JAN-2003. 98US-00163748.
XX
XX 30-SEP-1998; 98US-00163748.
XX
XX 30-SEP-1998; 98US-00163748.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX De Backer O, Van Den Eynde B, Boon-Falleur T;
XX
XX WPI; 2003-401119/38.
XX
XX P-PSDB; ADA15777.
XX
XX New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor
XX rejection antigen precursors, which complex to major histocompatibility
XX complex molecules to facilitate the proliferation of cytolytic T cells.
XX
XX Claim 1; Col 9-10; 15pp; English.
XX
XX The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the
XX nucleic acid molecules encoding them. The invention also relates to an
XX expression vector comprising an isolated nucleic acid molecule of the
XX invention operably linked to a promoter, a recombinant cell comprising
XX the isolated nucleic acid molecule or the expression vector and an
XX expression kit useful in generating cytolytic T lymphocytes (CTLs) or
XX determining if CTLs are present in a sample comprising the isolated
XX nucleic acid molecule and the isolated nucleic acid that encodes a human
XX leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid
XX molecules encode tumour rejection antigen precursors, which complex to
XX major histocompatibility complex (MHC) molecules to facilitate the
XX proliferation of cytolytic T cells. This sequence represents cDNA
XX encoding the human GAGE-7B polypeptide of the invention. The gene resides
XX on chromosome Xp11.2-p11.4.
XX
XX Sequence 526 BP; 168 A; 109 C; 143 G; 106 T; 0 U; 0 Other;
XX
XX Query Match 90.7%; Score 488; DB 7; Length 526;
XX Best Local Similarity 98.4%; Pred. No. 2e-131;
XX Matches 504; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
XX
XX 30 TGGTCTCGCGCTCGGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGT 89
XX
XX 1 TGGTCTCGCGCTCGGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGT 60
```

```
QY 90 TGGCGAGGAAGATCGACC---TATCGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAA 146
Db 61 TGGCGAGGAAGATCGACCTTATTTTGGCCCTAGACCAAGGCGCTATGTACAGCCTCCTGAA 120
QY 147 ATGATTGGGCCTATCGGCCCGAGCAGTTCAGTGAATGGAACCAACACCTGAA 206
Db 121 ATGATTGGGCCTATCGGCCCGAGCAGTTCAGTGAATGGAACCAACACCTGAA 180
QY 207 GAAGGGGAACCAAGCACTCAACGTCAAGATCCTGCAAGTCTCTCAGGAGGAGGATGAG 266
Db 181 GAAGGGGAACCAAGCACTCAACGTCAAGATCCTGCAAGTCTCTCAGGAGGAGGATGAG 240
QY 267 GGAGCATCTTCAGGTCAAGGGCGCAAGCCTGAAGCTCATAGCCAGGAACAGGGTCAACCA 326
Db 241 GGAGCATCTTCAGGTCAAGGGCGCAAGCCTGAAGCTCATAGCCAGGAACAGGGTCAACCA 300
QY 327 CAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGCGAGAGATGGACCCGCAAAATCCA 386
Db 301 CAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGCGAGAGATGGACCCGCAAAATCCA 360
QY 387 GAGGAGGTGAAAACGGCTGAAGAGGTGAAAAGCAATCACAGTGTAAAAGACACACGT 446
Db 361 GAGGAGGTGAAAACGGCTGAAGAGGTGAAAAGCAATCACAGTGTAAAAGAGGACACGT 420
QY 447 TGAATGATGCAGGCTGCTCTCTATGTTGGAAATTTGTTCAATTAATAATTCCTCCCAATAAAG 506
Db 421 TGAATGATGCAGGCTGCTCTCTATGTTGGAAATTTGTTCAATTAATAATTCCTCCCAATAAAG 480
QY 507 CTTTACAGCCTTCTGCAAGAAAAA 538
Db 481 CTTTACAGCCTTCTGCAAGAAAAA 512
```

```
RESULT 11
AAC02129
ID AAC02129 standard; cDNA; 430 BP.
XX
XX AAC02129;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein 5' EST, SEQ ID NO: 2127.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
XX
XX EPI033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX P-PSDB; AAG02123.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 1; SEQ ID NO 2127; 71pp + Sequence Listing; English.
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```
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
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DE	Human cancer agent-sensitive marker #227.	
XX	Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;	
KW	squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;	
KW	lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;	
KW	Hodgkin's disease; glioma; ss.	
XX	Homo sapiens.	
OS	WO200179556-A2.	
XX	25-OCT-2001.	
XX	13-APR-2001; 2001WO-US012132.	
PF	14-APR-2000; 2000US-0197538P.	
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
XX	Lillie J, Brown JL, Bolt A, Van Huffel C;	
PI	WPI; 2001-602933/68.	
XX	Novel nucleic acid, used as a marker to determine the effectiveness of	
XX	using TAXOL to treat cancer cell growth in individuals.	
PT	Claim 1; Page 231; 527pp; English.	
XX	The invention relates to 1046 novel nucleic acids which are used as	
CC	markers for determining the sensitivity of a cancer cell to the	
CC	anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they	
CC	are shown to express one of the 242 sensitivity markers or the cells are	
CC	shown not to express one of the 804 resistance markers. The methods can	
CC	be used to determine the effectiveness of TAXOL in the treatment of	
CC	cancer cell growth in an individual. The markers can be used as targets	
CC	in developing anti-cancer agents such as chemotherapeutic compounds. The	
CC	markers can also be used as targets in developing treatments for cancer,	
CC	particularly those cancers which display resistance to agents and exhibit	
CC	expression of the markers. The anticancer agents developed by the novel	
CC	method can be used to treat cancer. Probes based on the markers can be	
CC	used to detect transcripts or genomic sequences corresponding to the	
CC	markers, in the identification of cells or tissues which mis-express the	
CC	protein. Cancers which may be targeted include carcinoma (e.g. squamous	
CC	cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic	
CC	leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's	
CC	disease and tumours (e.g. glioma). The present sequence is one of the	
CC	1046 novel cancer cell markers	
XX	Sequence 365 BP; 63 A; 86 C; 66 G; 150 T; 0 U; 0 Other;	
SQ		
Query Match	55.6%; Score 299.2; DB 4; Length 365;	
Best Local Similarity	95.9%; Pred. No. 1.3e-76;	
Matches 307; Conservative	0; Mismatches 13; Indels 0; Gaps 0;	
Qy	219 GCAACTCAAGTCAGGATCTCTGAGCTGCTCAGGAGGAGAGGATGAGGAGCATGTGCA 278	
Db	365 GCAACTCAAGTCAGGATCTCTGAGCTGCTCAGGAGGAGAGGATGAGGAGCATGTGCA 306	
Qy	279 GGTCAGGGCCGAGCTGAGCTCATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 338	
Db	305 GGTCAGGGCCGAGCTGAGCTCATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 246	
Qy	339 GAGTGTGAAGATGCTCTGATGGGAGGAGATGGACCCGCAATCCAGAGAGGAGTGA 398	
Db	245 GAGTGTGAAGATGCTCTGATGGGAGGAGATGGACCCGCAATCCAGAGAGGAGTGA 186	
Qy	399 ACGGCTGAAGAGGTGAAAGCAATCA CAGTGTGTAAGAGAGACACGTTGAATGATGCA 458	
Db	185 ACGGCTGAAGAGGTGAAAGCAATCA CAGTGTGTAAGAGAGGCGCATGTTGAATGATGCA 126	
Qy	459 GGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAAGCTTTTACAGCTT 518	
Db	125 GGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAAGCTTTTACAGCTT 66	

QY	519 CTGCAAGAGAAAAA 538	
Db	65 CTAAGAAAAA 46	
RESULT 14		
ABZ19791		
ID	ABZ19791 standard; cDNA; 259 BP.	
XX	ABZ19791;	
AC	23-JAN-2003 (first entry)	
DT	Group III cDNA cancer related clone SEQ ID NO:2217.	
XX	Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;	
XX	immune response; virology; immunology; microbiology; molecular biology;	
KW	recombinant DNA technology; gene; ss.	
KW	Homo sapiens.	
OS	WO200278516-A2.	
XX	10-OCT-2002.	
XX	28-MAR-2002; 2002WO-US010421.	
XX	30-MAR-2001; 2001US-0280255P.	
PR	28-AUG-2001; 2001US-0315563P.	
PR	09-JAN-2002; 2002US-0347313P.	
XX	(CORI-) CORIXA CORP.	
PA	Wang T, Wang S, Bangur CS, Gaiger A;	
PI	WPI; 2003-058387/05.	
XX	New immunogenic polynucleotides or polypeptides useful for diagnosing,	
XX	preventing and treating cancer expressing CT or CP mRNA antigens, and in	
PT	PT virology, immunology, microbiology, molecular biology and recombinant DNA	
PT	techniques.	
XX	Claim 1; SEQ ID NO 2217; 207pp; English.	
PS	ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and	
CC	ABP54446 to ABP54472 represent protein (II) sequences, from the present	
CC	invention. (I) and (II) have cytostatic activity and can be used in gene	
CC	therapy and vaccines. (I), (II), antibodies and compositions from the	
CC	present invention are useful for diagnosing, preventing and treating	
CC	cancer, which expresses CT or CP mRNA antigens. They are useful for	
CC	stimulating immune response. They can also be useful in virology,	
CC	immunology, microbiology, molecular biology and recombinant DNA	
CC	techniques. N.B. The sequence data for this patent did not form part of	
CC	the printed specification, but was obtained in electronic format directly	
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences	
XX	Sequence 259 BP; 63 A; 65 C; 76 G; 55 T; 0 U; 0 Other;	
SQ		
Query Match	44.9%; Score 241.4; DB 7; Length 259;	
Best Local Similarity	99.6%; Pred. No. 6.8e-60;	
Matches 242; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 ACGCCAGGAGCTGTGAGGAGTCTGTGTGGTTCCTGCCGTCGGACTCTTTTCTCT 60	
Db	17 ACGCCAGGAGCTGTGAGGAGTCTGTGTGGTTCCTGCCGTCGGACTCTTTTCTCT 76	
Qy	61 ACTGAGATTCATCTGTGAAATATGATGGCCGAGAGATGACCTATCGGCTAGAC 120	
Db	77 ACTGAGATTCATCTGTGAAATATGATGGCCGAGAGATGACCTATCGGCTAGAC 136	
Qy	121 CAAGACGTAGTAGAGCTCTCGAAATGATTTGGGCTTATCGGCCCGCAGAGCTTCAGTG 180	





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2004, 09:51:18 ; Search time 2561 Seconds  
(without alignments)  
9105.253 Million cell updates/sec

Title: US-09-782-745-14

Perfect score: 538

Sequence: 1 ACGCAGGAGCTGTGAGC.....CTGCAAGAAAAA 538

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 3980872

Minimum DB seq length: 0

Maximum DB seq length: 538

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %		Length	DB	ID	Description
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2	538	100.0	538	6	BD231797	Isolated	BD231797 Isolated
3	538	100.0	538	6	I55851	Sequence 14	I55851 Sequence 14
4	538	100.0	538	6	BD132467	Isolated,	BD132467 Isolated,
5	530	98.5	530	9	HSU19143	Human GAGE-	U19143 Human GAGE-
6	525.4	97.7	528	6	AR275665	Sequence	AR275665 Sequence
7	525.4	97.7	528	9	AF055473	Homo sapi	AF055473 Homo sapi
8	504.8	93.8	532	6	AR028491	Sequence	AR028491 Sequence
9	504.8	93.8	532	6	BD231800	Isolated	BD231800 Isolated
10	504.8	93.8	532	6	I55854	Sequence 17	I55854 Sequence 17
11	504.8	93.8	532	6	BD132470	Isolated,	BD132470 Isolated,
12	501.4	93.2	528	6	AX334151	Sequence,	AX334151 Sequence,
13	501.4	93.2	528	9	HSU19145	Human GAGE-	U19145 Human GAGE-
14	498.6	92.7	527	9	HSU19147	Human GAGE-	U19147 Human GAGE-
15	497.6	92.5	524	9	AF058988	Homo sapi	AF058988 Homo sapi
16	496.8	92.3	524	9	HSU19146	Human GAGE-	U19146 Human GAGE-
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LOCUS	AR028488						
DEFINITION	AR028488						
ACCESSION	AR028488						
VERSION	AR028488.1	GI:5940461					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 538)						
AUTHORS	van der Bruggen, P., van den Bynde, B., DeBacker, O. and Boon-Falleur, T.						
TITLE	Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof						



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Best Local Similarity 100.0%; Pred. No. 2.6e-123;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 ACTGAGATTCATCTGTGTGAATATGAGTTGGCGAGAGATCGAATATCGGCTTAG 120
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QY 481 TGTTCATTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 538
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DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof.
ACCESSION BD132467
VERSION BD132467.1 GI:23227412
KEYWORDS JP 2002507112-A/7,
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 538)
AUTHORS Debacter, O., Eynde, B.V.D. and Falleur, T.B.
TITLE Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof
JOURNAL Patent: JP 2002507112-A 7 05-MAR-2002;
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH
PN JP 2002507112-A/7
PD 05-MAR-2002
PF 23-JUN-1997 JP 1998503430
PR 24-JUN-1996 US 08/669161
PI OLIVIER DEBACTER, BENOIT VAN DEN EYNDE, THIERRY BOON, FALLEUR PC
A61K38/00, A61K45/05, C07K7/00, C07K14/82, C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Best Local Similarity 100.0%; Pred. No. 2.6e-123;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ACGCCAGGAGCTGTGAGGAGCTGTGTTGTTCTCGCGTCCGCGTCTTTTCTCT 60
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RESULT 5
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DEFINITION Human GAGE-2 protein mRNA, complete cds.
ACCESSION U19143
VERSION U19143.1 GI:914900
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 530)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S. and Boon, T.
JOURNAL A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma
MEDLINE J. Exp. Med. 182 (3), 689-698 (1995)
PUBMED 95378788
REFERENCE 2 (bases 1 to 530)
AUTHORS Van den Eynde, B.J.
TITLE Direct Submission
JOURNAL Submitted (28-DEC-1994) Benoit J Van Den Eynde, Ludwig Institute For Cancer Research, 74 Avenue Hippocrate, BRUSSELS, 1200, BELGIUM
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/mol_type="mRNA"
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sex="female"

cell\_line="M2-MEL.43"

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dev\_stage="adult"

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codon\_start=1

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protein\_id="AA82745.1"

db\_xref="GI:914901"

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EVKIPREGKQSQ"

Query Match

Best Local Similarity 98.5%; Score 530; DB 9; Length 530;

Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

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60

Db

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60

QY

61

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120

Db

61

ACTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATCGGCTAGAC

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QY

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Db

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QY

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QY

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RESULT 6

AR275665

LOCUS

DEFINITION

Sequence

AR275665

ACCESSION

AR275665.1

GI:29709167

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 528)

De Backer, O., Van den Eynde, B. and Boon-Palleur, T.

TITLE

Isolated, truncated nucleic acid which are members of the gage, and

uses thereof

JOURNAL

Patent: US 6509172-A 1 21-JAN-2003;

FEATURES

Location/Qualifiers

1..528

source

db\_xref="taxon:9606"

sex="female"

cell\_line="M2-MEL.43"

tissue\_type="melanoma"

dev\_stage="adult"

84..434

codon\_start=1

product="GAGE-2 protein"

protein\_id="AA82745.1"

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translation="MSWRGSTRVPRPRRYVEPEMIGMPRPFQSDVEVPATPERGE  
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EVKIPREGKQSQ"

Query Match

Best Local Similarity 98.5%; Score 530; DB 9; Length 530;

Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

1

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60

QY

61

ACTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATCGGCTAGAC

120

Db

61

ACTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATCGGCTAGAC

120

QY

121

CAAGACGCTACGTAGAGCTCTCTGAAATGATTTGGGCTTATCGGCGGAGAGCTTCACT

180

Db

121

CAAGACGCTACGTAGAGCTCTCTGAAATGATTTGGGCTTATCGGCGGAGAGCTTCACT

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QY

181

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QY

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Db

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TGTTCAATTAATTCCTCCCAATAAAGCTTTACAGCTTCTGCAAGAGAAA 530

RESULT 6

AR275665

LOCUS

DEFINITION

Sequence

AR275665

ACCESSION

AR275665.1

GI:29709167

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 528)

De Backer, O., Van den Eynde, B. and Boon-Palleur, T.

TITLE

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JOURNAL

Patent: US 6509172-A 1 21-JAN-2003;

FEATURES

Location/Qualifiers

1..528

source

db\_xref="taxon:9606"

sex="female"

cell\_line="M2-MEL.43"

tissue\_type="melanoma"

dev\_stage="adult"

84..434

codon\_start=1

product="GAGE-2 protein"

protein\_id="AA82745.1"

db\_xref="GI:914901"

translation="MSWRGSTRVPRPRRYVEPEMIGMPRPFQSDVEVPATPERGE  
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120

Db

61

ACTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATCGGCTAGAC

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QY

121

CAAGACGCTACGTAGAGCTCTCTGAAATGATTTGGGCTTATCGGCGGAGAGCTTCACT

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Db

121

CAAGACGCTACGTAGAGCTCTCTGAAATGATTTGGGCTTATCGGCGGAGAGCTTCACT

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QY

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TGTTCAATTAATTCCTCCCAATAAAGCTTTACAGCTTCTGCAAGAGAAA 530

RESULT 6

AR275665

LOCUS

DEFINITION

Sequence

AR275665

ACCESSION

AR275665.1

GI:29709167

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 528)

De Backer, O., Van den Eynde, B. and Boon-Palleur, T.

TITLE

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JOURNAL

Patent: US 6509172-A 1 21-JAN-2003;

FEATURES

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source

db\_xref="taxon:9606"

sex="female"

cell\_line="M2-MEL.43"

tissue\_type="melanoma"

dev\_stage="adult"

84..434

codon\_start=1

product="GAGE-2 protein"

protein\_id="AA82745.1"

db\_xref="GI:914901"

translation="MSWRGSTRVPRPRRYVEPEMIGMPRPFQSDVEVPATPERGE  
PATCRQDPAARQGBEDGASAGQPKPEAHSQGHQPTGCECEBDGPDGEMDPNPE  
EVKIPREGKQSQ"

Query Match

Best Local Similarity 100.0%; Pred. No. 2.5e-121;

Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

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240

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QY

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QY

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QY

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Db

481

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RESULT 6

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LOCUS

DEFINITION

Sequence

AR275665

ACCESSION

AR275665.1

GI:29709167

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 528)

De Backer, O., Van den Eynde, B. and Boon-Palleur, T.

TITLE

Isolated, truncated nucleic acid which are members of the gage, and

uses thereof

JOURNAL

Patent: US 6509172-A 1 21-JAN-2003;

FEATURES

Location/Qualifiers

1..528

source

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cell\_line="M2-MEL.43"

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dev\_stage="adult"

84..434

codon\_start=1

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db\_xref="GI:914901"

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EVKIPREGKQSQ"

Query Match

Best Local Similarity 99.8%; Pred. No. 3.5e-120;

Matches 526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

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71

Db

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60

QY

72

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131

Db

61

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120

QY

132

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Db

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QY

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251

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240

QY

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311

Db

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QY

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371

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QY

372

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431

Db

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QY

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480

QY

492

ATTCTCCCAATAAAGCTTTACAGCTTCTGCAAGAGAAA 538

Db

481

ATTCTCCCAATAAAGCTTTACAGCTTCTGCAAGAGAAA 527

RESULT 7

AF055473

LOCUS

DEFINITION

Homo sapiens GAGE-8 mRNA, complete cds.

ACCESSION

AF055473

VERSION

AF055473.1

GI:3511022

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 528)

De Backer, O., Arden, K.C., Boret, M., Vantomme, V., De Smet, C.,

AUTHORS

Czekay, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van den

TITLE

Characterization of the GAGE genes that are expressed in various

JOURNAL

human cancers and in normal testis

MEDLINE

Cancer Res. 59 (13), 3157-3165 (1999)

PUBMED

99323388

REFERENCE

2 (bases 1 to 528)

De Backer, O.R.Y.

AUTHORS

Direct Submission

TITLE

Submitted (24-MAR-1998) Ludwig Institute for Cancer Research,

JOURNAL

Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium

FEATURES

Location/Qualifiers

1..528

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/organism="Homo sapiens"

db\_xref="taxon:9606"

sex="female"

cell\_line="M2-MEL.43"

tissue\_type="melanoma"

dev\_stage="adult"

84..434

codon\_start=1

product="GAGE-2 protein"

protein\_id="AA82745.1"

db\_xref="GI:914901"

translation="MSWRGSTRVPRPRRYVEPEMIGMPRPFQSDVEVPATPERGE  
PATCRQDPAARQGBEDGASAGQPKPEAHSQGHQPTGCECEBDGPDGEMDPNPE  
EVKIPREGKQSQ"

Query Match

Best Local Similarity 97.7%; Score 525.4; DB 6; Length 528;

Matches 526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

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71

Db

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TCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATCGGCTAGACCAAGACGCTAC

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QY

132

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Db

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QY

192

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QY

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QY

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QY

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431

Db

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GACCGCCCAATCCAGAGGAGGTGAAACCGCTCAAGAGGTGAAAGCAATCAAGTGT

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QY

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491

Db

421

TAAAGAGAGACACCTTGAATATGATGAGGCTGCTCTATGTTGAAATTTGTTCAATTA

480

QY

492

ATTCTCCCAATAAAGCTTTACAGCTTCTGCAAGAGAAA 538

Db

481

ATTCTCCCAATAAAGCTTTACAGCTTCTGCAAGAGAAA 527

RESULT 7

AF055473

LOCUS

DEFINITION

Homo sapiens GAGE-8 mRNA, complete cds.

ACCESSION

AF055473

VERSION

AF055473.1

GI:3511022

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 528)

De Backer, O., Arden, K.C., Boret, M., Vantomme, V., De Smet, C.,

AUTHORS

Czekay, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van den

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Characterization of the GAGE genes that are expressed in various

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human cancers and in normal testis

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JOURNAL

Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium

FEATURES

Location/Qualifiers

1..528

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/organism="Homo sapiens"

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cell\_line="M2-MEL.43"

tissue\_type="melanoma"

dev\_stage="adult"

84..434

codon\_start=1

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PATCRQDPAARQGBEDGASAGQPKPEAHSQGHQPTGCECEBDGPDGEMDPNPE  
EVKIPREGKQSQ"

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Best Local Similarity 99.8%; Pred. No. 3.5e-120;

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QY

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ATTCTCCCAATAAAGCTTTACAGCTTCTGCAAGAGAAA 538

Db

481

ATTCTCCCAATAAAGCTTTACAGCTTCTGCAAGAGAAA 527

RESULT 7

AF055473

LOCUS

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VERSION

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GI:3511022

KEYWORDS

Homo sapiens (human)

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Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 528)

De Backer, O., Arden, K.C., Boret, M., Vantomme, V., De Smet, C.,

AUTHORS

Czekay, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van den

TITLE

Characterization of the GAGE genes that are expressed in various

JOURNAL

human cancers and in normal testis

MEDLINE

Cancer Res. 59 (13), 3157-3165 (1999)

PUBMED

99323388

REFERENCE

2 (bases 1 to 528)

De Backer, O.R.Y.

AUTHORS

Direct Submission

TITLE

Submitted (24-MAR-1998) Ludwig Institute for Cancer Research,

JOURNAL

Brussels Branch, 74 av. Hippocrate



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EVKPEEGKQSQC"

ORIGIN
Query Match 97.7%; Score 525.4; DB 9; Length 528;
Best Local Similarity 99.8%; Pred. No. 3.5e-120;
Matches 526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 372 GACCGCCCAATTCAGAGAGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAAGTGT 431
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Db 481 ATTCTCCCAATTAAGCTTTACAGCTTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 527

RESULT 8
AR028491
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 532)
AUTHORS
Bruggen,P.V.D., Eynde,B.V.D., DeBacker,O. and Falleur,T.B.
TITLE
Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
as molecules encoding the same, and utilization thereof
JOURNAL
Patent: US 5858689-A 17 12-JAN-1999;
C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC STRANDEDNESS:single,TOPOLOGY:linear
FH Key Location/Qualifiers

/mol_type="mRNA"
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ORIGIN
Query Match 93.8%; Score 504.8; DB 6; Length 532;
Best Local Similarity 98.1%; Pred. No. 4.8e-115;
Matches 522; Conservative 0; Mismatches 7; Indels 3; Gaps 1;
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RESULT 9
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 532)
AUTHORS
Bruggen,P.V.D., Eynde,B.V.D., DeBacker,O. and Falleur,T.B.
TITLE
Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
as molecules encoding the same, and utilization thereof
JOURNAL
Patent: JP 2002509859-A 10 02-APR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT
OS Homo sapiens (human)
PN JP 2002509859-A/10
PD 02-APR-2002
PF 12-JAN-1999 JP 2000528586
PR 23-JAN-1998 US 09/012818
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,
THIERRY BOON FALLEUR
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC STRANDEDNESS:single,TOPOLOGY:linear
FH Key Location/Qualifiers
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    Best Local Similarity 98.1%; Pred. No. 4.8e-115;
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RESULT 11
LOCUS BD132470 532 bp DNA linear PAT 18-SEP-2002
DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor
ACCESSION BD132470
VERSION BD132470.1 GI:23227415
KEYWORDS JP 2002507112-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 532)
AUTHORS DeBacker,O., Eynde,B.V.D. and Falleur,T.B.
TITLE Isolated, nucleic acid molecules which code for GAGE tumor
JOURNAL rejection antigen, the tumor rejection antigen, and uses thereof
COMMENT Patent: JP 2002507112-A 10 05-MAR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
PN JP 2002507112-A/10
PD 05-MAR-2002
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PR 24-JUN-1996 US 08/669161
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A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 CC
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CC Topology: Linear;
FH Key Location/Qualifiers.
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DEFINITION Sequence 17 from patent US 5648226.
ACCESSION I55854
VERSION I55854.1 GI:2476648
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 532)
AUTHORS Van den Eynde,B., DeBacker,O. and Boon-Falleur,T.
TITLE Isolated peptides derived from tumor rejection antigens, and their
JOURNAL use
COMMENT Patent: US 5648226-A 17 15-JUL-1997;
LUDWIG INSTITUTE FOR CANCER RESEARCH
PN US 5648226-A/1
PD 15-JUL-1997
PF 15-JUL-1997
PR 15-JUL-1997
PI .
A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 CC
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    QY 127 GCTACGTAGAGCTCTGTAATGATTGGGCTATGCGGCCGAGCAGTTCAGTGTGAAG 186
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U19145.1 GI:914904
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S.
and Boon,T.
A new family of genes coding for an antigen recognized by
autologous cytolytic T lymphocytes on a human melanoma
J. Exp. Med. 182 (3), 689-698 (1995)
95378788
PUBMED
7544395
REFERENCE
2 (bases 1 to 528)
Van Den Eynde,B.J.
Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
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VERSION	U19147.1
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REFERENCE	1 (bases 1 to 527)
AUTHORS	Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S. and Boon, T.
TITLE	A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma
JOURNAL	J. Exp. Med. 182 (3), 689-698 (1995)
MEDLINE	95378788
PUBMED	7544395
REFERENCE	2 (bases 1 to 527)
AUTHORS	Van den Eynde, B.J.
TITLE	Direct Submission
JOURNAL	Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium.
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ACCESSION	AF058988
VERSION	AF058988.1
KEYWORDS	GI:3300089
SOURCE	Human sapiens (human)
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AUTHORS	1 (bases 1 to 524)
TITLE	Chen, M.E., Lin, S.-H., Chung, L.W.K. and Sikes, R.A. Isolation and characterization of PAGE-1 and GAGE-7: new genes expressed in the lncap prostate cancer progression model that share homology with melanoma associated antigens
JOURNAL	J. Biol. Chem. (1998) In press
REFERENCE	2 (bases 1 to 524)

AUTHORS Chen, M.E., Lin, S.-H., Chung, L.W.K. and Sikes, R.A.  
TITLE Direct Submission  
JOURNAL Submitted (07-APR-1998) Urology, University of Virginia, Box 422,  
Charlottesville, VA 22908, USA

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QY	242	AGCTGTCTCAGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCTGAAGC	301
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Job time : 2567 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY\_NUC  
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 4080270

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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4	560	100.0	560	6	BD132468	BD132468 Isolated,
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7	446.4	79.7	532	6	BD231800	BD231800 Isolated
8	446.4	79.7	532	6	I55854	I55854 Sequence 17
9	446.4	79.7	532	6	BD132470	BD132470 Isolated,
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11	443.2	79.1	526	9	AF055474	AF055474 Homo sapi
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ALIGNMENTS

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LOCUS	AR028489	Sequence 15 from patent US 5856689.			
DEFINITION	AR028489				
ACCESSION	AR028489.1	GI:5940462			
VERSION	AR028489.1				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 560)				
AUTHORS	van der Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Falleur,T.				
TITLE	Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof				

JOURNAL Patent: US 5858689-A 15 12-JAN-1999;

## FEATURES

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1. .560  
LOCATION/Qualifiers

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Query Match	100.0%;	Score 560;	DB 6;	Length 560;
Best Local Similarity	100.0%;	Pred. No. 7.3e-137;		
Matches 560;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CTCATATTTTCACACAGATGATGGCGAGGAAGATCGACCTATTATTGGTCTAGGCCCAAT	60	
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QY	61	AATAGGTCGATCTTCTCGCAACTCATATTTTCACACAGATGAATCTCAGTAGAGGAAA	120	
Db	61	AATAGGTCGATCTTCTCGCAACTCATATTTTCACACAGATGAATCTCAGTAGAGGAAA	120	
QY	121	TCGACCTATTATTGGCCTAGACCAAGCGCTATGTATACGCTCTCTGAAGTGATTTGGGCCT	180	
Db	121	TCGACCTATTATTGGCCTAGACCAAGCGCTATGTATACGCTCTCTGAAGTGATTTGGGCCT	180	
QY	181	ATCGGGCCCGAGCAGTTTCAGTGATGAAGTGAACCCAGCAACACCTGAAGAGGGGAACCA	240	
Db	181	ATCGGGCCCGAGCAGTTTCAGTGATGAAGTGAACCCAGCAACACCTGAAGAGGGGAACCA	240	
QY	241	GCAACTCAACGTACAGATCTCTGCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGCA	300	
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QY	301	GGTCAAGGGCCGAGCGCTGAAGCTGTAGCCAGCAACAGGTGTACCCACAGACTTGGGTGT	360	
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QY	361	GAGTGTGAAGATGGTCTCTGATGGCAGGAGATGGACCCGCAAAATCCAGAGAGGTGAAA	420	
Db	361	GAGTGTGAAGATGGTCTCTGATGGCAGGAGATGGACCCGCAAAATCCAGAGAGGTGAAA	420	
QY	421	ACGCTTGAAAGAGGTGAAAAGCAATCACAGTGTTTAAAAGAGGCACGTTGAAATGATGCA	480	
Db	421	ACGCTTGAAAGAGGTGAAAAGCAATCACAGTGTTTAAAAGAGGCACGTTGAAATGATGCA	480	
QY	481	GGCTGCTCTTATGTTGAAAATTTGTCATTTAAAATTTCTCCCAATAAAGCTTTTACAGCCTT	540	
Db	481	GGCTGCTCTTATGTTGAAAATTTGTCATTTAAAATTTCTCCCAATAAAGCTTTTACAGCCTT	540	
QY	541	CTGCAAGAAAAAATAAAAAA	560	
Db	541	CTGCAAGAAAAAATAAAAAA	560	

RESULT 2	
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LOCUS	560 bp DNA linear PAT 17-JUL-2003
DEFINITION	Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof.
ACCESSION	BD231798
VERSION	BD231798.1 GI:33041568
KEYWORDS	JP 2002509859-A/8.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1. (bases 1 to 560)
TITLE	Bruggen, P.V.D., Eynde, B.V.D., Debacker, O. and Falleur, T.B.
JOURNAL	Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof
COMMENT	Patent: JP 2002509859-A 8 02-APR-2002; LUDWIG INSTITUTE FOR CANCER RESEARCH OS Homo sapiens (human) PN JP 2002509859-A/8 PD 02-APR-2002

PF	12-JAN-1999	JP	2000528586	
PR	23-JAN-1998	US	09/012818	
PI	PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE, OLIVIER DEBACKER,			
PI	THIERRY BOON FALLEUR			
PC	C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00	CC		
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CC	Topology: Linear;			
CC	STRANDEDNESS:single,TOPOLOGY:linear			
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	Best Local Similarity	100.0%;	Pred. No. 7,3e-137;	
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Qy	61	AATAGTTCGATCTTCTCCCACTCATATTTACACACAGATGAATCTCAGTAGAGAAA	120	
Db	61	AATAGTTCGATCTTCTCCCACTCATATTTACACACAGATGAATCTCAGTAGAGAAA	120	
Qy	121	TCGACCTATTATTGGCCTAGACCAAGCGCTATGTACAGCCTCCTCAAGTGAATGGGCCT	180	
Db	121	TCGACCTATTATTGGCCTAGACCAAGCGCTATGTACAGCCTCCTCAAGTGAATGGGCCT	180	
Qy	181	ATCGGCGCCGAGCAGTTCTAGTGAAGTGGAAACAGCAACACCTGAAGAAGGGGAACCA	240	
Db	181	ATCGGCGCCGAGCAGTTCTAGTGAAGTGGAAACAGCAACACCTGAAGAAGGGGAACCA	240	
Qy	241	GCAACTCAACGTCAGGATCTCGACGTGCTCAGGAGGAGAGGATCAGGAGGATCTGCA	300	
Db	241	GCAACTCAACGTCAGGATCTCGACGTGCTCAGGAGGAGAGGATCAGGAGGATCTGCA	300	
Qy	301	GGTCAAGGCGGAGGCTGAACTGATAGCAGGAACAGGTCACCAAGCTGGGTGT	360	
Db	301	GGTCAAGGCGGAGGCTGAACTGATAGCAGGAACAGGTCACCAAGCTGGGTGT	360	
Qy	361	GAGTGTCAAGATGTCCTGATGGCAGGAGATCGACCCGCAATCCAGAGGAGGTGAAA	420	
Db	361	GAGTGTGAAGATGTCCTGATGGCAGGAGATCGACCCGCAATCCAGAGGAGGTGAAA	420	
Qy	421	ACGCCCTGAAGAAGGTGAAAAGCAATCACAGTGTAAAAAGAGGACGTTGAAATGATGCA	480	
Db	421	ACGCCCTGAAGAAGGTGAAAAGCAATCACAGTGTAAAAAGAGGACGTTGAAATGATGCA	480	
Qy	481	GGCTGCTCCTATGTTGGAAATTTGTTCAATAAAATTTCCCAATAAGCTTTACAGCCTT	540	
Db	481	GGCTGCTCCTATGTTGGAAATTTGTTCAATAAAATTTCCCAATAAGCTTTACAGCCTT	540	
Qy	541	CTGCAAGAAGAAAAA	560	
Db	541	CTGCAAGAAGAAAAA	560	
RESULT 3				
LOCUS	I55852		560 bp	DNA linear PAT 07-OCT-1997
DEFINITION	Sequence 15 from patent US 5648226.			
ACCESSION	I55852			
VERSION	I55852.1		GI:2476646	
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			



REFERENCE 1 (bases 1 to 560)  
AUTHORS Van den Eynde,B., DeBacker,O. and Boon-Falleur,T.  
TITLE Isolated peptides derived from tumor rejection antigens, and their use  
JOURNAL Patent: US 5648226-A 15 15-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..560  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 560; DB 6; Length 560;  
Best Local Similarity 100.0%; Pred. No. 7.3e-137;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCATATTTCACACAGATGAGTTGGCGAGGAAGATCGACCTATTATTGCTTAGGCCAAT 60  
Db 1 CTCATATTTCACACAGATGAGTTGGCGAGGAAGATCGACCTATTATTGCTTAGGCCAAT 60  
QY 61 AATAGTTCGATCTTCTCGCCCACTCATATTTTCACACAGATGAATCTCAGTAGAGGAAA 120  
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Db 541 CTGCAAGAAAAA 560  
RESULT 4  
BD132468  
LOCUS BD132468 560 bp DNA linear PAT 18-SEP-2002  
DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof.  
ACCESSION BD132468  
VERSION BD132468.1 GI:23227413  
KEYWORDS JP 2002507112-A/8.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 560)  
AUTHORS Debacker,O., Eynde,B.V.D. and Falleur,T.B.  
TITLE Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof  
JOURNAL Patent: JP 2002507112-A 8 05-MAR-2002;  
LUDWIG INSTITUTE FOR CANCER RESEARCH

COMMENT PN JP 2002507112-A/8  
PD 05-MAR-2002  
PF 23-JUN-1997 JP 1998503430  
PR 24-JUN-1996 US 08/669161  
PI OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIERRY BOON FALLEUR PC  
A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 560; DB 6; Length 560;  
Best Local Similarity 100.0%; Pred. No. 7.3e-137;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCATATTTCACACAGATGAGTTGGCGAGGAAGATCGACCTATTATTGCTTAGGCCAAT 60  
Db 1 CTCATATTTCACACAGATGAGTTGGCGAGGAAGATCGACCTATTATTGCTTAGGCCAAT 60  
QY 61 AATAGTTCGATCTTCTCGCCCACTCATATTTTCACACAGATGAATCTCAGTAGAGGAAA 120  
Db 61 AATAGTTCGATCTTCTCGCCCACTCATATTTTCACACAGATGAATCTCAGTAGAGGAAA 120  
QY 121 TCGACCTATTATTGGCTTAGACCAAGCGCTATGTACAGCCTCCTGAAGTGATTGGGCT 180  
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QY 361 GAGTGTGAAGATGGTCTGATGGCGAGAGATGGACCCGCCAAATCCAGAGAGGTGAAA 420  
Db 361 GAGTGTGAAGATGGTCTGATGGCGAGAGATGGACCCGCCAAATCCAGAGAGGTGAAA 420  
QY 421 ACGCTGTGAAGAGGTGAAAAGCAATCACAGTGTCTTAAAGAGAGGCACGTTGAATGATCA 480  
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QY 481 GGCTGCTCTATGTTGGAAATTTGTTTCATTAATAATTTCTCCCAATAAAGCTTTACAGCCTT 540  
Db 481 GGCTGCTCTATGTTGGAAATTTGTTTCATTAATAATTTCTCCCAATAAAGCTTTACAGCCTT 540  
QY 541 CTGCAAGAAAAA 560  
Db 541 CTGCAAGAAAAA 560  
RESULT 5  
HSU19144  
LOCUS HSU19144 552 bp mRNA linear PRI 04-DEC-1995  
DEFINITION Human GAGE-3 protein mRNA, complete cds.  
ACCESSION U19144  
VERSION U19144.1 GI:914902  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 552)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S. and Boon, T.

TITLE A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma

J. Exp. Med. 182 (3), 689-698 (1995)

MEDLINE 95378788

PUBMED 7544395

REFERENCE 2 (bases 1 to 552)

AUTHORS Van den Eynde, B.J.

TITLE Direct Submission

JOURNAL Submitted (28-DEC-1994) Benoit J Van den Eynde, Ludwig Institute For Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium

FEATURES

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/sex="female"

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98..68; Score 552; DB 9; Length 552;

Query Match 98.6%; Score 552; DB 9; Length 552;

Best Local Similarity 100.0%; Pred. No. 9.4e-135; Indels 0; Gaps 0;

Matches 552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCATATTTCACAGATGAGTTGCGGAGGAAGATCGACCTATTATTATTGGTCTAGGCCAAT 60

DB 1 CTCATATTTCACAGATGAGTTGCGGAGGAAGATCGACCTATTATTATTGGTCTAGGCCAAT 60

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DB 61 AATAGTTCGATCTTCCTGCCCACTCATATTTCACAGATGATCTCAGTAGAGGAAA 120

QY 121 TCGACCTATTATTGGCTTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGAATTGGCGCT 180

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QY 181 ATGCGGCCGAGCAGTTCAGTGTGAATGGAAACCAACACCTGAAGAGGGGAACCA 240

DB 181 ATGCGGCCGAGCAGTTCAGTGTGAATGGAAACCAACACCTGAAGAGGGGAACCA 240

QY 241 GCACTCAACGTTCAGGATCTCTGAGCTGCTCAGGAGGAGGATGAGGAGCATCTGCA 300

DB 241 GCACTCAACGTTCAGGATCTCTGAGCTGCTCAGGAGGAGGATGAGGAGCATCTGCA 300

QY 301 GGTCAAGGCCGAGACCTGAACTGATAGCCAGAAACAGGCTCACCCACAGACTGGGTGT 360

DB 301 GGTCAAGGCCGAGACCTGAACTGATAGCCAGAAACAGGCTCACCCACAGACTGGGTGT 360

QY 361 GAGTGTGAAGATGTCTCTGATGGGAGAGATGAGATGAGCCGCCCAATCCAGAGGAGTGA 420

DB 361 GAGTGTGAAGATGTCTCTGATGGGAGAGATGAGATGAGCCGCCCAATCCAGAGGAGTGA 420

QY 421 ACGCTCAAGAGGTGAAAGCAATCAAGTGTAAAGAGGACAGCTTGAAATGATGCA 480

DB 421 ACGCTCAAGAGGTGAAAGCAATCAAGTGTAAAGAGGACAGCTTGAAATGATGCA 480

QY 481 GGCTGCTCTTATGTTGGAATTTGTTTCAATTAATTTCTCCCAATTAAGCTTTTACAGCCTT 540

DB 481 GGCTGCTCTTATGTTGGAATTTGTTTCAATTAATTTCTCCCAATTAAGCTTTTACAGCCTT 540

QY 541 CTGCAAGAAAA 552

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Db 541 CTGCAAGAAAA 552

RESULT 6

AR028491

LOCUS

DEFINITION Sequence 17 from patent US 5858689.

ACCESSION AR028491

VERSION AR028491.1 GI:5940464

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 532)

AUTHORS van der Bruggen, P., van den Eynde, B., DeBacker, O. and Boon-Falleur, T.

TITLE Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof

JOURNAL Patent: US 5858689-A 17 12-JAN-1999;

FEATURES

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ORIGIN

Query Match 79.7%; Score 446.4; DB 6; Length 532;

Best Local Similarity 99.8%; Pred. No. 7e-107; Indels 0; Gaps 0;

Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 113 GAGGAAAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172

DB 85 GAGGAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 144

QY 173 TTGGGCTTATGCGGCCGACGAGTTTCAGTGAAGTGAACCAACGACCTGAAGAAG 232

DB 145 TTGGGCTTATGCGGCCGACGAGTTTCAGTGAAGTGAACCAACGACCTGAAGAAG 204

QY 233 GGGAAACAGCAACTCAACGTCAGGATCCTCAGCTCCTCAGGAGGAGAGATGAGGAG 292

DB 205 GGGAAACAGCAACTCAACGTCAGGATCCTCAGCTCCTCAGGAGGAGAGATGAGGAG 264

QY 293 CATCTGAGGTCAAGGCCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCAACCCACAGA 352

DB 265 CATCTGAGGTCAAGGCCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCAACCCACAGA 324

QY 353 CTGGTGTGAGTGTGAAGATGCTCCTGATGGGAGGAGATGGACCCCAATCCAGAG 412

DB 325 CTGGTGTGAGTGTGAAGATGCTCCTGATGGGAGGAGATGGACCCCAATCCAGAG 384

QY 413 AGGTGAAAACGCTCTGAAGAGGTGAAAAGCAATCACAGTGTGTTAAAGAGGACGTTGAA 472

DB 385 AGGTGAAAACGCTCTGAAGAGGTGAAAAGCAATCACAGTGTGTTAAAGAGGACGTTGAA 444

QY 473 ATGATGAGGCTGCTCTCTATGTTGGAAATTTGTTTCAATTAATTTCTCCCAATTAAGCTTT 532

DB 445 ATGATGAGGCTGCTCTCTATGTTGGAAATTTGTTTCAATTAATTTCTCCCAATTAAGCTTT 504

QY 533 ACAGCTTCTGCAAGAAAAA 560

DB 505 ACAGCTTCTGCAAGAAAAA 532

RESULT 7

BD231800

LOCUS

DEFINITION Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof.

ACCESSION BD231800

VERSION BD231800.1 GI:33041570

KEYWORDS JP 2002509859-A/10.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Vertebrata; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.  
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 Best Local Similarity 99.8%; Pred. No. 7e-107;  
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCCTCAAGTGA 172  
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 QY 173 TTGGGCTTATCGGCCCGAGCAGTTTCAGTGTAGTGAAGTGAACACCAACACCTGAAGAAG 232  
 DB 145 TTGGGCTTATCGGCCCGAGCAGTTTCAGTGTAGTGAAGTGAACACCAACACCTGAAGAAG 204  
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 DB 205 GGGAAACCACTCAACCTCAAGCTCAGATCTGATGAAGTGAACACCAACACCTGAAGAAG 264  
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 DB 265 CATCTGCAGGTCAAGGGCCGAGCAGTTTCAGTGTAGTGAAGTGAACACCAACACCTGAAGAAG 324  
 QY 353 CTGGGTGTGAGTGTGAAGTGTCTCTGATGGCGAGGATGGACCCGCCAAATCCAGAGG 412  
 DB 325 CTGGGTGTGAGTGTGAAGTGTCTCTGATGGCGAGGATGGACCCGCCAAATCCAGAGG 384  
 QY 413 AGGTGAAACCCCTCAAGAGGTGAAAGCAATCACAGTGTAAAGAGGCAAGTGTAA 472  
 DB 385 AGGTGAAACCCCTCAAGAGGTGAAAGCAATCACAGTGTAAAGAGGCAAGTGTAA 444  
 QY 473 ATGATGAGGCTGTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAGCTTT 532  
 DB 445 ATGATGAGGCTGTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAGCTTT 504  
 QY 533 ACAGCTTCTGCAAGAGAAAAA 560  
 DB 505 ACAGCTTCTGCAAGAGAAAAA 532

RESULT 10  
 AR275666  
 LOCUS AR275666 526 bp DNA linear PAT 10-APR-2003  
 DEFINITION Sequence 2 from patent US 6509172.  
 ACCESSION AR275666  
 VERSION AR275666.1 GI:29709168  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 526)  
 AUTHORS De Backer, O., Van den Eynde, B. and Boon-Falleur, T.  
 TITLE Isolated, truncated nucleic acid which are members of the gage, and uses thereof  
 JOURNAL Patent: US 6509172-A 2 21-JAN-2003;  
 FEATURES  
 source  
 1..526  
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## ORIGIN

Query Match 79.1%; Score 443.2; DB 6; Length 526;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-106;  
 Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCCTCAAGTGA 172

DB 65 GAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCCTCAAGTGA 124  
 QY 173 TTGGGCTTATCGGCCCGAGCAGTTTCAGTGTAGTGAAGTGAACACCAACACCTGAAGAAG 232  
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 QY 233 GGGAAACCACTCAACCTCAAGCTCAGATCTGATGAAGTGAACACCAACACCTGAAGAAG 292  
 DB 185 GGGAAACCACTCAACCTCAAGCTCAGATCTGATGAAGTGAACACCAACACCTGAAGAAG 244  
 QY 293 CATCTGCAGGTCAAGGGCCGAGCAGTTTCAGTGTAGTGAAGTGAACACCAACACCTGAAGAAG 352  
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 QY 353 CTGGGTGTGAGTGTGAAGTGTCTCTGATGGCGAGGATGGACCCGCCAAATCCAGAGG 412  
 DB 305 CTGGGTGTGAGTGTGAAGTGTCTCTGATGGCGAGGATGGACCCGCCAAATCCAGAGG 364  
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 DB 365 AGGTGAAACCCCTCAAGAGGTGAAAGCAATCACAGTGTAAAGAGGCAAGTGTAA 424  
 QY 473 ATGATGAGGCTGTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAGCTTT 532  
 DB 425 ATGATGAGGCTGTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAGCTTT 484  
 QY 533 ACAGCTTCTGCAAGAGAAAAA 560  
 DB 485 ACAGCTTCTGCAAGAGAAAAA 512

## RESULT 11

AF055474  
 LOCUS AF055474 526 bp mRNA linear PRI 01-MAY-2000  
 DEFINITION Homo sapiens GAGE-7B mRNA, complete cds.  
 ACCESSION AF055474  
 VERSION AF055474.1 GI:3511024  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 526)  
 AUTHORS De Backer, O., Arden, K.C., Boretti, M., Vantomme, V., De Smet, C., Czekey, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van den Eynde, B., Boon, T. and van der Bruggen, P.  
 TITLE Characterization of the GAGE genes that are expressed in various human cancers and in normal testis  
 JOURNAL Cancer Res. 59 (13), 3157-3165 (1999)  
 MEDLINE 99323388  
 PUBMED 10397259  
 REFERENCE 2 (bases 1 to 526)  
 AUTHORS De Backer, O.R.Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-MAR-1998) Ludwig Institute for Cancer Research, Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium  
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DEFINITION Sequence 16 from patent US 5858689.
ACCESSION AR028490
VERSION AR028490.1 GI:5940463
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS van der Bruggen,P., van den Eynde,B., DeBacker,O. and
Boon-Falleur,T.
TITLE Isolated peptides derived from the gage tumor rejection antigen
JOURNAL Precursor and uses thereof
PATENT: US 5858689-A 16 12-JAN-1999;
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DEFINITION Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
as molecules encoding the same, and utilization thereof.
ACCESSION BD231799
VERSION BD231799.1 GI:33041569
KEYWORDS JP 2002509859-A/9.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS 1 (bases 1 to 540)
Bruggen,P.V.D., Eynde,B.V.D., Debacker,O., and Falleur,T.B.
TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
as molecules encoding the same, and utilization thereof
JOURNAL Patent: JP 2002509859-A 9 02-APR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT OS Homo sapiens (human)
PN JP 2002509859-A/9
PD 02-APR-2002
PF 12-JAN-1999 JP 2000528586
PR 23-JAN-1998 US 09/012818
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,
THIERRY BOON FALLEUR
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ACCESSION I55853  
VERSION I55853.1 GI:2476647  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 540)  
AUTHORS Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.  
TITLE Isolated peptides derived from tumor rejection antigens, and their use  
JOURNAL  
PATENT: US 5648226-A 16 15-JUL-1997;  
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DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof.  
ACCESSION BD132469  
VERSION BD132469.1 GI:23227414  
KEYWORDS JP 2002507112-A/9.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 540)  
AUTHORS Debacker, O., Eynde, B. V. D. and Falleur, T. B.  
TITLE Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof  
JOURNAL Patent: JP 2002507112-A 9 05-MAR-2002;  
LUDWIG INSTITUTE FOR CANCER RESEARCH  
COMMENT PN JP 2002507112-A/9  
PD 05-MAR-2002  
PF 23-JUN-1997 JP 1998503430  
PI 24-JUN-1996 US 08/669161  
A61K38/00, A61K45/05, C07K7/00, C07K14/82, C12N15/00 CC  
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Job time : 2563 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)

5940.611 Million cell updates/sec

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 30620086

Minimum DB seq length: 0

Maximum DB seq length: 560

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

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28: gb\_gsl:\*

29: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C	12	405.4	72.4	455	9	AI187350
C	13	404.6	72.2	509	12	BI868671
C	14	398.8	71.2	426	9	AA868226
	15	374	66.8	505	14	CB115693
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VERSION BM832793  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 537)  
AUTHORS Kim,K.J., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.  
TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
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        of EcoRI which site is also included in vector. An RNA
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        The obtained cDNA vectors were used for transformation of
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        After analyzing and sequencing about 2,000 ~ 3,000
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        selected and amplified by PCR reaction using vector region
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        synthesis of biotinylated single stranded RNA by in vitro
        transcription reaction. The synthesized RNA probes were
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        from original library and incubated with avidin-gel.
        After removing DNA-RNA hybrids by centrifuge, the
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    Query Match      78.8%; Score 441.2; DB 12; Length 537;
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 VERSION BG120336.1 GI:12613845  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 480)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: ggapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
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 http://image.llnl.gov  
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 DB 1 GAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCTCCTGAAGTGTG 60  
 QY 176 GGCCTATGCGGCCGAGCAGTTCAGTGAAGTGGAACCGAGCAACCTCGAAGAGGG 235  
 DB 61 GGCCTATGCGGCCGAGCAGTTCAGTGAAGTGGAACCGAGCAACCTCGAAGAGGG 120  
 QY 236 AACACGCAACTCAAGCTCAGATCCTGAGTGTGATGAAGTGGAACCGAGCAACCTCGAAGAGGG 295  
 DB 121 AACACGCAACTCAAGCTCAGATCCTGAGTGTGATGAAGTGGAACCGAGCAACCTCGAAGAGGG 180  
 QY 296 CTGAGGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGACTG 355  
 DB 181 CTGAGGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGACTG 240  
 QY 356 GGTGTGAGTGTGAAGATGGTCTGATGGGCGAGGATGGACCCGCCAAATCCAGAGGAGG 415  
 DB 241 GGTGTGAGTGTGAAGATGGTCTGATGGGCGAGGATGGACCCGCCAAATCCAGAGGAGG 300  
 QY 416 TGAAGACCGCTGAAAGAGGTGAAAGCAATCAAGTGTGTTAAAGAGGACAGCTTGAATG 475  
 DB 301 TGAAGACCGCTGAAAGAGGTGAAAGCAATCAAGTGTGTTAAAGAGGACAGCTTGAATG 360

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QY 476 ATGAGGCTCTCTATGTTGGAATTTCTTCAATTAATAATTCCTCCCAATAAAGCTTTTACA 535
Db 361 ATGAGGCTCTCTCTATGTTGGAATTTCTTCAATTAATAATTCCTCCCAATAAAGCTTTTACA 420
QY 536 GCCTTCTGCAAAAGAAAAA 560
Db 421 GCCTTCTGCAAAAGAAAAA 445

RESULT 3
BX108227
LOCUS
DEFINITION
  BX108227 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE998K213161 ;
  IMAGE:1256204, mRNA sequence.
ACCESSION
  BX108227
VERSION
  BX108227.1 GI:27835080
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 521)
  Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
  Radelof,U., Schneider,D. and Korn,B.
  Human Unigeneset - RZPD3
  Unpublished (2003)
  Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
  RZPD; IMAG998K213161.
  RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
  http://www.rzpd.de/CloneCards/cgi-
  bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Heubnerweg 6, D-14059 Berlin, Germany
  Tel: +49 30 32639 101
  Fax: +49 30 32639 111
  www.rzpd.de
  This clone is available royalty-free from RZPD;
  contact RZPD (clone@rzpd.de) for further information. Seq primer:
  M13r, Primer sequence: TTTCACAGCAAGAACAGCTAGAC.
FEATURES
  source
    1..521
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    /db_xref="taxon:9606"
    /clone="IMAG998K213161 ; IMAGE:1256204"
    /tissue_type="pooled germ cell tumors"
    /lab_host="DH10B"
    /clone_lib="NCI_CGAP_GC3"
    /note="Vector: pT73D-Pac (Pharmacia) with a modified
    polylinker; 1st strand cDNA was prepared from 3 pooled
    germ cell tumors, and was then primed with a Not I -
    oligo(dT) primer. Double-stranded cDNA was ligated to Eco
    RI adaptors (Pharmacia), digested with Not I and cloned
    into the Not I and Eco RI sites of the modified pT73
    vector. Library is not normalized. Library was
    constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
  Query Match 77.6%; Score 434.8; DB 13; Length 521;
  Best Local Similarity 98.4%; Pred. No. 6.8e-86;
  Matches 439; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 113 GAGGAAATTCGACCTATTATTCGCTAGACCAAGCGCTATCTACAGCCTCTCTGAAGTGA 172
Db 75 GAGGAGATCGACCTGTTATTGGCTAGTCCCAAGCGCTATCTACAGCCTCTCTGAAGTGA 134
QY 173 TTGGGCTATCGGCGCCGAGCGTTTCAGTGTGAAGTGAACCAACACCTGAAGAAG 232
Db 135 TTGGGCTATCGAGCCGAGCGATTTCAGTGTGAAGTGAACCAACACCTGAAGAAG 194

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QY 233 GGGAAACCGACAACTCAAGTCAAGATCCCTGACGTGCTCAGAGGAGAGGATGAGGGAG 292
Db 195 GGGAAACCGACAACTCAAGTCAAGATCCCTGACGTGCTCAGAGGAGAGGATGAGGGAG 254
QY 293 CATCTGCAAGTCAAGGGCGGAGCCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 352
Db 255 CATCTGCAAGTCAAGGGCGGAGCCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 314
QY 353 CTGGGTGTGAGTGTGAAGATGCTCTGATGGCGAGAGATGACCCGCCAAATCCAGAGG 412
Db 315 CTGGGTGTGAGTGTGAAGATGCTCTGATGGCGAGAGATGACCCGCCAAATCCAGAGG 374
QY 413 AGGTGAAAACGCTGAAGAGAGGTGAAAAGCAATCAAGTGTAAAGAGGACCGTTGAA 472
Db 375 AGGTGAAAACGCTGAAGAGAGGTGAAAAGCAATCAAGTGTAAAGAGGACCGTTGAA 434
QY 473 ATGATGCAAGGCTGCTCTATGTTGAAATTTCTTCAATTAATAATTCCTCCCAATAAAGCTTT 532
Db 435 ATGATGCAAGGCTGCTCTATGTTGAAATTTCTTCAATTAATAATTCCTCCCAATAAAGCTTT 494
QY 533 ACAGCCTTCTGCAAAAGAAAAA 558
Db 495 ACAGCCTTCTGCAAAAGAAAAA 520

RESULT 4
AI381509/c
LOCUS
DEFINITION
  AI381509.1 447 bp mRNA linear EST 28-MAR-1999
  te76b07.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
  IMAGE:2092597 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;
  mRNA sequence.
ACCESSION
  AI381509
VERSION
  AI381509.1 GI:4194290
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 447)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  This clone is available royalty-free through LLNL ; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Insert Length: 497 Std Error: 0.00
  Seq primer: -40UP from Gibco.
FEATURES
  Location/Qualifiers
    1..447
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:2092597"
    /lab_host="DH10B"
    /clone_lib="Soares NFL T GBC S1"
    /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
    a modified polylinker; Site 1: Not I; Site 2: Eco RI;
    Equal amounts of plasmid DNA from three normalized
    libraries (fetal lung NDHL19W, testis NHT, and B-cell
    NCI CGAP GCBI) were mixed, and ss circles were made in
    vitro. Following HAP purification, this DNA was used as
    tracer in a subtractive hybridization reaction. The driver
    was PCR-amplified cDNAs from pools of 5,000 clones made
    from the same 3 libraries. The pools consisted of
    I.M.A.G.E. clones 297480-302087, 682632-687239,
    726408-728711, and 729096-731399. Subtraction by Bento
    Soares and M. Fatima Bonaldo. "
ORIGIN
  Query Match 77.6%; Score 434.6; DB 9; Length 447;

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Best Local Similarity 99.1%; Pred. No. 7.5e-86; Matches 437; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 113 GAGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172  
Db 441 GAGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 382

QY 173 TTGGGCTATGCGGCCGAGCAGTTCACTGATGAAGTGGAAACCAAGCAACACCTGAAGAAG 232  
Db 381 TTGGGCTATGCGGCCGAGCAGTTCACTGATGAAGTGGAAACCAAGCAACACCTGAAGAAG 322

QY 233 GGGAAACAGCAACTCAACGTCAGGATCCTCGAGCTCTCGAGGCGGAGAGGAGGAG 292  
Db 321 GGGAAACAGCAACTCAACGTCAGGATCCTCGAGCTCTCGAGGCGGAGAGGAGGAG 262

QY 293 CATCTGAGGTCAGGCGGAGCCTCAACGTCAGGATCCTCGAGCTCTCGAGGCGGAGAGGAGGAG 352  
Db 261 CATCTGAGGTCAGGCGGAGCCTCAACGTCAGGATCCTCGAGCTCTCGAGGCGGAGAGGAGGAG 202

QY 353 CTGGGTCGAGTGTGAAGATGGTCTCATGGGAGGAGATGGACCCGCCAAATCCAGAGG 412  
Db 201 CTGGGTCGAGTGTGAAGATGGTCTCATGGGAGGAGATGGACCCGCCAAATCCAGAGG 142

QY 413 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTAAAGAGGAGGAGGAGGAGGAG 472  
Db 141 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTAAAGAGGAGGAGGAGGAGGAG 82

QY 473 ATGATGAGGCTGCTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAGCTTT 532  
Db 81 ATGATGAGGCTGCTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAGCTTT 22

QY 533 ACAGCTTCTGCAAGAAAAA 553  
Db 21 ACAGCTTCTGCAAGAAAAA 1

RESULT 5  
AW510753/c  
LOCUS  
DEFINITION h39D05.x1 Soares NFL\_T GBC\_S1 Homo sapiens cDNA clone IMAGE:2911881 3' similar to SW:GGE4\_HUMAN Q13068 GAGE-4 PROTEIN. ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW510753  
AW510753.1 GI:7148831  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 457)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: -40UP from Gibco.  
Location/Qualifiers  
1. .457  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2911881"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-CCGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as

FEATURES  
source

tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

Query Match 77.4%; Score 433.6; DB 10; Length 457;  
Best Local Similarity 99.1%; Pred. No. 1.3e-85; Matches 436; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 113 GAGAAATCGACCTATTATTGGCCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172  
Db 440 GAGAAATCGACCTATTATTGGCCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 381

QY 173 TTGGGCTATGCGGCCGAGCAGTTCACTGATGAAGTGGAAACCAAGCAACACCTGAAGAAG 232  
Db 380 TTGGGCTATGCGGCCGAGCAGTTCACTGATGAAGTGGAAACCAAGCAACACCTGAAGAAG 321

QY 233 GGGAAACAGCAACTCAACGTCAGGATCCTCGAGCTCTCGAGGCGGAGAGGAGGAG 292  
Db 320 GGGAAACAGCAACTCAACGTCAGGATCCTCGAGCTCTCGAGGCGGAGAGGAGGAG 261

QY 293 CATCTGAGGTCAGGCGGAGCCTCAACGTCAGGATCCTCGAGCTCTCGAGGCGGAGAGGAGGAG 352  
Db 260 CATCTGAGGTCAGGCGGAGCCTCAACGTCAGGATCCTCGAGGCGGAGAGGAGGAG 201

QY 353 CTGGGTCGAGTGTGAAGATGGTCTCATGGGAGGAGATGGACCCGCCAAATCCAGAGG 412  
Db 200 CTGGGTCGAGTGTGAAGATGGTCTCATGGGAGGAGATGGACCCGCCAAATCCAGAGG 141

QY 413 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTAAAGAGGAGGAGGAGGAGGAG 472  
Db 140 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTAAAGAGGAGGAGGAGGAG 81

QY 473 ATGATGAGGCTGCTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAGCTTT 532  
Db 80 ATGATGAGGCTGCTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAGCTTT 21

QY 533 ACAGCTTCTGCAAGAAAAA 552  
Db 20 ACAGCTTCTGCAAGAAAAA 1

## RESULT 6

AA738037/c  
LOCUS  
DEFINITION AA738037 464 bp mRNA linear EST 22-JAN-1998  
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AA738037  
AA738037.1 GI:2768794  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 464)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Suck, M.D., Ph.D.  
cDNA Library preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bhrp/image/image.html](http://www-bio.llnl.gov/bhrp/image/image.html)  
Insert length: 511 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 435.  
Location/Qualifiers  
1. .464  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1256204"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GC3"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
Query Match 77.1%; Score 432; DB 9; Length 464;  
Best Local Similarity 97.1%; Pred. No. 2.8e-85;  
Matches 438; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 113 GAGGAAATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGA 172  
Db |||||  
QY 454 GAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGA 395  
Db |||||  
QY 173 TTGGGCTATGCGGCCGAGCGAGTTCAGTGTGAAGTGAAGCAACACCTGAAGAG 232  
Db |||||  
QY 394 TTGGGCTATGCGGCCGAGCGAGTTCAGTGTGAAGTGAAGCAACACCTGAAGAG 335  
Db |||||  
QY 233 GGGACCCGCACTCAACTCAGGATCTCTGACGCTCTCAGAGGAGGAGTGAAGGAG 292  
Db |||||  
QY 334 GGGACCCGCACTCAACTCAGGATCTCTGACGCTCTCAGAGGAGGAGTGAAGGAG 275  
Db |||||  
QY 293 CATCTGCAGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 352  
Db |||||  
QY 274 CATCTGCAGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 215  
Db |||||  
QY 353 CTGGGTGTGAAGTGTGAAGTGTCTCTGATGGCAGGAGATGACCGCCCAATCCAGAG 412  
Db |||||  
QY 214 CTGGGTGTGAAGTGTGAAGTGTCTCTGATGGCAGGAGATGACCGCCCAATCCAGAG 155  
Db |||||  
QY 413 AGGTGAAACGCTCAAGAGAGTGAAGCAATCACTGTTTAAAGAGGACAGTTGAA 472  
Db |||||  
QY 154 AGGTGAAACGCTCAAGAGAGTGAAGCAATCACTGTTTAAAGAGGACAGTTGAA 95  
Db |||||  
QY 473 ATGATGCAGGCTGCTCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAGAGTTT 532  
Db |||||  
QY 94 ATGATGCAGGCTGCTCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAGAGTTT 35  
Db |||||  
QY 533 ACAGCCTTCTGCAAGAAAAA 560  
Db |||||  
QY 34 ACAGCCTTCTGCAAGAAAAA 7  
Db |||||

RESULT 7  
B1826605  
LOCUS  
DEFINITION  
B1826605 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5168892 5',  
mRNA sequence.  
ACCESSION  
B1826605.1 GI:15938155  
VERSION  
EST.  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 527)  
AUTHORS  
NIH-MGC <http://mgc.mci.nih.gov/>.  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11419 row: p column: 13  
High quality sequence stop: 519.

FEATURES  
source

Location/Qualifiers  
1. .527  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:5168892"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_119"  
/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 76.6%; Score 429.2; DB 12; Length 527;  
Best Local Similarity 99.1%; Pred. No. 1.2e-84;  
Matches 442; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 113 GAGGAAATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGA 172  
Db |||||  
QY 83 GAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGA 142  
Db |||||  
QY 173 TTGGGCTATGCGGCCGAGCGAGTTCAGTGTGAAGTGAAGCAACACCTGAAGAG 232  
Db |||||  
QY 143 TTGGGCTATGCGGCCGAGCGAGTTCAGTGTGAAGTGAAGCAACACCTGAAGAG 202  
Db |||||  
QY 233 GGGACCAAGCAACTCAAGTCAAGATCTCTGAGCTCTCAGAGGGAGAGGATGAGGAG 292  
Db |||||  
QY 203 GGGACCAAGCAACTCAAGTCAAGATCTCTGAGCTCTCAGAGGGAGAGGATGAGGAG 262  
Db |||||  
QY 293 CATCTGCAGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 352  
Db |||||  
QY 263 CATCTGCAGTCAAGGGCCGAGGCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 322  
Db |||||  
QY 353 CTGGGTGTGAAGTGTGAAGTGTCTCTGATGGCGAGGATGAGCCCGCAATCCAGAGG 412  
Db |||||  
QY 323 CTGGGTGTGAAGTGTGAAGTGTCTCTGATGGCGAGGATGAGCCCGCAATCCAGAGG 382  
Db |||||  
QY 413 AGGTGAAACGCTCAAGAGTGAAGCAATCACTGTTTAAAGAGGACAGTTGAA 472  
Db |||||  
QY 383 AGGTGAAACGCTCAAGAGTGAAGCAATCACTGTTTAAAGAGGACAGTTGAA 442  
Db |||||  
QY 473 ATGATGCAGGCTGCTCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAGAGTTT 532  
Db |||||  
QY 443 ATGATGCAGGCTGCTCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAGAGTTT 502  
Db |||||  
QY 533 ACAGCCTTCTGCAAGAAAAA 558  
Db |||||  
QY 503 ACAGCCTTCTGCAAGAAAAA 527  
Db |||||

RESULT 8  
CF780547  
LOCUS  
DEFINITION  
AGENCOURT\_15739102 NIH\_MGC\_217 Homo sapiens cDNA clone

CF780547 517 bp mRNA linear EST 20-OCT-2003  
AGENCOURT\_15739102 NIH\_MGC\_217 Homo sapiens cDNA clone

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IMAGE:30524555 5', mRNA sequence.
CF780547 1 GI:37739989
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 517)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gcapbs-i@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
cDNA Library Preparation by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM604 row: e column: 12
High quality sequence stop: 517.
FEATURES
source
location/Qualifiers
1..517
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524555"
/tissue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_217"
/notes="Vector: pVX-Asc; Site 1: EcoRI; Site 2: NotI;
Library is oligo-dT primed and directionally cloned.
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to rRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pVX-Asc vector. Average insert size
0.5-1kb. Adaptors 5' (AATTCGGCAGGAG)3' and 5'd
(CCTCGGCG)3'. 3' linker sequence - GCGCGCTCAGAGCC T18.
Sequencing primers 3' end: T3 promoter primer 5'd
(AATACCTCAGTAAAGGGA)3'. 5' End: T7 promoter primer 5'd
(TAATACGACTCACTAGGG)3'. Average insert size 0.5-1kb.
Library was constructed in the laboratory of M. Bento
Soares. Note: this is a NIH_MGC Library."
ORIGIN
Query Match 76.5%; Score 428.2; DB 14; Length 517;
Best Local Similarity 99.3%; Pred. No. 2e-84;
Matches 430; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 113 GAGGAATTCAGCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172
Db 84 GAGGAATTCAGCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 143
Qy 173 TTGGGCTATGCGGCCGAGCAGTTCAAGTGTAGTGAAGTGAAGTGAAGTGAAGTGAAG 232
Db 144 TTGGGCTATGCGGCCGAGCAGTTCAAGTGTAGTGAAGTGAAGTGAAGTGAAGTGA 203
Qy 233 GGGACCGGACCTCAAGCTCAGATCTGAGTCTCAGAGGAGGAGATGAGGAG 292
Db 204 GGGACCGGACCTCAAGCTCAGATCTGAGTCTCAGAGGAGGAGATGAGGAG 263
Qy 293 CATCTGAGGTCAAGGGCGGAGCCTGAGTGTAGTGAAGTGAAGTGAAGTGAAGTGAAG 352
Db 264 CATCTGAGGTCAAGGGCGGAGCCTGAGTGTAGTGAAGTGAAGTGAAGTGAAGTGA 323
Qy 353 CTGGGTGTGTGAGTGTGAGTGTCTGTGTGGCAGGAGATGGACCCGCCAATTCAGAGG 412

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324 CTGGGTGTGAGTGTGAAGATGTCCTGATGGCGAGGATGGACCCGCCAAATCCAGAGG 383
Qy 413 AGGTGAAACGCTCTGAAGAGGTGAAGCAATCACAGTGTAAAGAGGACGCGTTGAA 472
Db 384 AGGTGAAACGCTCTGAAGAGGTGAAGCAATCACAGTGTAAAGAGGACGCGTTGAA 443
Qy 473 ATGATCAGGCTCTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAAGCTTT 532
Db 444 ATGATCAGGCTCTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCCAATAAAGCTTT 503
Qy 533 ACAGCCTTCTGCA 545
Db 504 ACAGCCTTCTGCA 516

RESULT 9
AA447559/c
LOCUS
DEFINITION
AA447559 489 bp mRNA linear EST 04-JUN-1997
zw81el1.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:782636
3' similar to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ; mRNA
sequence.
ACCESSION
AA447559
VERSION
AA447559.1 GI:2161229
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 489)
REFERENCE
AUTHORS
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Scheilenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 427.
FEATURES
source
location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:782636"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
TGTTACCAATCTGAAGTGGGCGCGCCCAATTTTTTTTTTTTTTTT 3' ].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match 75.7%; Score 423.8; DB 9; Length 489;
Best Local Similarity 99.3%; Pred. No. 1.9e-83;
Matches 436; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 113 GAGGAATTCAGCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172

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438 GAGGAAGATCGACCTATTATTGTCCTAGACCAAGCGCTATGTACAGCCTCTGAAGTGA 379  
173 TTGGGCTATCGGCGCCGAGCAGTTCAGTGAATGAAGTGAACAGCAACACCTGAAGAAG 232  
378 TT-GGCCTATCGGCGCCGAGCAGTTCAGTGAATGAAGTGAACAGCAACACCTGAAGAAG 320  
233 GGGAAACAGCACTCAACGTCAGAGTCTGACGCTCTCAGGAGGAGGAGGAG 292  
319 GGGAAACAGCACTCAACGTCAGAGTCTGACGCTCTCAGGAGGAGGAGGAG 260  
293 CATCTGCAGTCAAGGCGCCGAGCCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 352  
259 CATCTGCAGTCAAGGCGCCGAGCCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 200  
353 CTGGGTGTGAGTGTGAAGTGTCTGATGGGAGGAGATGACCCGCGCAATCCAGAGG 412  
199 CTGGGTGTGAGTGTGAAGTGTCTGATGGGAGGAGATGACCCGCGCAATCCAGAGG 140  
413 AGGTGAAACCGCTGAAGAGGTGAAGCAATCACAGTGTAAAGAGGAGGAGGAGTGA 472  
139 AGGTGAAACCGCTGAAGAGGTGAAGCAATCACAGTGTAAAGAGGAGGAGGAGTGA 80  
473 ATGATGAGGCTGCTCTATGTTGGAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532  
79 ATGATGAGGCTGCTCTATGTTGGAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 20  
533 ACAGCCTCTGCAAAAGAAA 551  
19 ACAGCCTCTGCAAAAGAAA 1

RESULT 10  
AA760996/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
AA760996 450 bp mRNA linear EST 26-JAN-1998  
mx32n08.s1 NCI\_CGAP GC4 Homo sapiens cDNA clone IMAGE:1257855 3',  
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.  
AA760996  
AA760996.1 GI:2809926  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 450)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: -40m3 fwd. ET from Amersham  
High quality sequence stop: 331.  
Location/Qualifiers  
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/clone="IMAGE:1257855"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP GC4"  
/note="Vector: pVT3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pVT3  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 75.0%; Score 420; DB 9; Length 450;  
Best Local Similarity 98.4%; Pred. No. 1.3e-82;  
Matches 434; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 113 GAGGAAATCGACCTATTATTGCGCTAGACCAAGCGCTATGTACAGCCTCTGAAGTGA 172  
Db 440 GAGGAAATCGACCTATTATTGCGCTAGACCAAGCGCTATGTACAGCCTCTGAAGTGA 381  
QY 173 TTGGGCTATCGGCGCCGAGCAGTTCAGTGAATGAAGTGAACAGCAACACCTGAAGAAG 232  
Db 380 NTGTGCTATGCGCGCCGAGCAGTTCAGTGAATGAAGTGAACAGCAACACCTGAAGAAG 321  
QY 233 GGGAAACAGCACTCAACGTCAGAGTCTGACGCTCTCAGGAGGAGGAGGAG 292  
Db 320 GGGAAACAGCACTCAACGTCAGAGTCTGACGCTCTCAGGAGGAGGAGGAG 261  
QY 293 CATCTGCAGTCAAGGCGCCGAGCCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 352  
Db 260 CATCTGCAGTCAAGGCGCCGAGCCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGA 201  
QY 353 CTGGGTGTGAGTGTGAAGTGTCTGATGGGAGGAGATGACCCGCGCAATCCAGAGG 412  
Db 200 CTGGGTGTGAGTGTGAAGTGTCTGATGGGAGGAGATGACCCGCGCAATCCAGAGG 141  
QY 413 AGGTGAAACCGCTGAAGAGGTGAAGCAATCACAGTGTAAAGAGGAGGAGGAGTGA 472  
Db 140 AGGTGAAACCGCTGAAGAGGTGAAGCAATCACAGTGTAAAGAGGAGGAGGAGTGA 81  
QY 473 ATGATGAGGCTGCTCTATGTTGGAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532  
Db 80 ATGATGAGGCTGCTCTATGTTGGAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 22  
QY 533 ACAGCCTCTGCAAAAGAAA 553  
Db 21 ACAGCCTCTGCAAAAGAAA 1

RESULT 11  
AA760996/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
AA760996 418 bp mRNA linear EST 10-SEP-1999  
UI-H-B10p-abg-g-06-0-UI.s1 NCI\_CGAP\_Sub2 Homo sapiens cDNA clone  
IMAGE:2711986 3', mRNA sequence.  
AA760996  
AA760996.1 GI:5865303  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 418)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: M13 Forward  
POLYA=Yes.  
Location/Qualifiers

FEATURES

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/clone="IMAGE:2711986"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Sub2"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NCI CGAP Sub2 library is a subtracted library derived from
BI. BI constitutes a mixture of 21 normalized or
subtracted NCI CGAP libraries: NCI CGAP Co4,
NCI CGAP Pr22, NCI CGAP P-28, NCI CGAP Co10,
NCI CGAP Co16, NCI CGAP Kid5, NCI CGAP Kid12,
NCI CGAP Kid3, NCI CGAP Kid11, NCI CGAP Lym2,
NCI CGAP Br2, NCI CGAP Co8, NCI CGAP CL11, NCI CGAP Lei2,
NCI CGAP Brn23, NCI CGAP Lu5, NCI CGAP Lu24,
NCI CGAP Brn23, NCI CGAP Lu5, NCI CGAP GC6, NCI CGAP Brn25.
These 21 libraries were pooled and a single-stranded DNA
preparation of the resulting mixture was used as a tracer
in a subtractive hybridization with a driver whose
composition is detailed below: NCI CGAP Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids
1322376-1323911, 1456008-1456775, 1500552-1502855)
NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clonoids 1323912-1325831, 1471368-1472903,
1492104-1493255) NCI CGAP Lu5 pool 1 LLAM 3575-3582,
3851-3854 (IMAGE Clonoids 1414920-1417991,
1520904-1522439) NCI CGAP GC4 pool 1 LLAM 3164-3167,
3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631,
1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids
985608-986759, 1101192-1101959, 1217928-1220615)
NCI CGAP Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
Clonoids 1057416-1061255, 1144584-1145351) The resulting
subtracted library contained 4 million recombinants.
Subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.
TAG_TISSUE=germ cell
TAG_LIB=NCI CGAP_GC4
TAG_SEQ=AAATC"

ORIGIN
Query Match 72.7%; Score 407.4; DB 9; Length 418;
Best Local Similarity 98.6%; Pred. No. 7.8e-80;
Matches 411; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 144 AAGCGCTATGTACAGCTCTGTAAGTGAATGGGCTATGGCGCCGAGCACTTCAGTGA 203
Db 418 AAGAGCTTACGTAGAGCTCTCTGAATGATTTGGGCTATGGCGCCGAGCACTTCAGTGA 359
Qy 204 TGAAGTGAACACGACCACTGAAGAGGGGAACACGACACTCAACGTCAGTACCTGTC 263
Db 358 TGAAGTGAACACGACCACTGAAGAGGGGAACACGACACTCAACGTCAGTACCTGTC 299
Qy 264 AGCTGCTCAGAGGGAGGAGTGGGAGGATCTGCAGTCAAGGGCGGAGCTCGAAGC 323
Db 298 AGCTGCTCAGAGGGAGGAGTGGGAGGATCTGCAGTCAAGGGCGGAGCTCGAAGC 239
Qy 324 TGATAGCCAGGAACAGGGGTACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGTATGG 383
Db 238 TCATAGCCAGGACAGGGTACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGTATGG 179
Qy 384 GCAGAGATGACCCCGCAATTCAGAGAGGTGAACCGCTGAAGAGGTGAAGACA 443
Db 178 GCAGAGATGACCCCGCAATTCAGAGAGGTGAACCGCTGAAGAGGTGAAGACA 119
Qy 444 ATCAGAGTGAAGAGAGGACGTTGAAGTATGACAGGCTGCTCCTATGTTGAAATTT 503
Db 118 ATCAGAGTGAAGAGAGGACGTTGAAGTATGACAGGCTGCTCCTATGTTGAAATTT 59
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504 GTTCATTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 560
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58 GTTCATTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 2
|||||

Al187350 455 bp mRNA linear EST 10-NOV-1998
qf29a05.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1751408
3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. [1] ; mRNA
sequence.
Al187350
Al187350.1 GI:3737988
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapsb@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 504 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 391.
Location/Qualifiers
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/db_xref="taxon:9606"
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/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTTTTTT 3'.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5 and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 72.4%; Score 405.4; DB 9; Length 455;
Best Local Similarity 97.1%; Pred. No. 2.2e-79;
Matches 434; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

Qy 113 GAGGAAATCGACCTATTATTGGCCTAGACCAAGCGCTATGTACAGCTCTCGAAGTGA 172
Db 445 GAGGAAATGACCTATTATTGGCCTAGA-CAAGCGCTATGT-CAGCTCTCGAAGTGA 388
Qy 173 TTGGGCTATCGCGCCCGCAGGAGTTCAGTGTGAAGTGGACCAACCTCCTGAAGAG 232
Db 387 TTGGGCTATCGCGCCCGCAGGAGTTCAGTGTGAAGTGGACCAACCTCCTGAAGAG 328
Qy 233 GGGAAACAGCAACTCAACGTCAGGATCTCGAGCTGTCTCAGAGGGAGAGGATGAGGAG 292
Db 327 GGGAAACAGCAACTCAACGTCAGGATCTCGAGCTGTCTCAGAGGGAGAGGATGAGGAG 268
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QY 293 CATCTGAGGTCAAGGCCCAAGCCTGAAGCTGATACCCAGGAACAGGCTCACCCACAGA 352
Db 267 CATCTGAGTCAAGGCCCAAGCCTGAAGCTGATACCCAGGAACAGGCTCACCCACAGA 208
QY 353 CTGGGTGTGAGTGAAGATGGTCTCTGATGGCAGGAGATGGACCCGCCCAATCCAGAGG 412
Db 207 CTGGGTGTGAGTGAAGATGGTCTCTGATGGCAGGAGATGGACCCGCCCAATCCAGAGG 148
QY 413 AGGTGAAAACCGCTGAGAGAGGTGAAGCAATCACAGTGTATAAGAGAGGCGAGTTGAA 472
Db 147 AGGTGAAAACCGCTGAGAGAGGTGAAGCAATCCAGTGTATAAGAGAGGCGAGTTGAA 88
QY 473 ATGATGAGGCTGCTCCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532
Db 87 ATGATGAGGCTGCTCCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 28
QY 533 ACAGCCTTCTGCAAAAGAAAAA 559
Db 27 CCAGCCTTCTGCAAAAGAAAAA 1

RESULT 13
LOCUS BI868671
DEFINITION 603392594F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5',
mRNA sequence.
ACCESSION BI868671
VERSION BI868671.1 GI:16042344
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL2026 row: 1 column: 24
High quality sequence stop: 509.
FEATURES
Location/Qualifiers
1..509
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/clone="IMAGE:5402663"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 72.2%; Score 404.6; DB 12; Length 509;
Best Local Similarity 99.0%; Pred. No. 3.3e-79;
Matches 407; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTCGCTAGACCAAGGCGCTATGACAGCCTCTGAGTGA 172
Db 99 GAGGAAATCGACCTATTATTCGCTAGACCAAGGCGCTATGACAGCCTCTGAGTGA 158
QY 173 TTGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGAACACAGCAACCTGAAGAG 232

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Db 159 TTGGGCTATGCGGCCCGAGCAGTTCAAGTGAACACAGCAACCTGAAGAG 218
QY 233 GGAACACAGCAACTCAACGTCAGGATCCCTGACGCTCAGGAGGAGAGGATGAGGAG 292
Db 219 GGAACACAGCAACTCAACGTCAGGATCCCTGACGCTCAGGAGGAGAGGATGAGGAG 278
QY 293 CATCTGAGGTCAAGGCCCAAGCCTGAAGCTGATACCCAGGAACAGGCTCACCCACAGA 352
Db 279 CATCTGAGGTCAAGGCCCAAGCCTGAAGCTCATAGCCAGGAACAGGCTCACCCACAGA 338
QY 353 CTGGGTGTGAGTGAAGATGGTCTCTGATGGCAGGAGATGGACCCGCCCAATCCAGAGG 412
Db 339 CTGGGTGTGAGTGAAGATGGTCTCTGATGGCAGGAGATGGACCCGCCCAATCCAGAGG 398
QY 413 AGGTGAAAACCGCTGAGAGAGGTGAAGCAATCACAGTGTATAAGAGAGGCGAGTTGAA 472
Db 399 AGGTGAAAACCGCTGAGAGAGGTGAAGCAATCACAGTGTATAAGAGAGGCGAGTTGAA 458
QY 473 ATGATGAGGCTGCTCCTATGTTGGAAATTTGTTCAATTAATTTCTCCCA 523
Db 459 ATGATGAGGCTGCTCCTATGTTGGAAATTTGTTCAATTAATTTCTCCCA 509

RESULT 14
LOCUS AA868226/c
DEFINITION ak48h07.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1409245
3', similar to SW:GGE2_HUMAN Q13066 GAGE-2 PROTEIN. [1] ;, mRNA
sequence.
ACCESSION AA868226
VERSION AA868226.1 GI:2963671
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 363.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:1409245"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/notes="Vector: pT73-Pac (Pharmacia) with a modified
polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5]
TGTACCAATCTGAAGTGGAGCGGCCCAATTTTTTTTTTTTTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library

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went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

/clone lib="L8SCK0"  
/note="Organ: Liver; Vector: pT73-Pac; Site 1: EcoRI; Site 2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

ORIGIN  
Query Match 71.2%; Score 398.8; DB 9; Length 426;  
Best Local Similarity 96.7%; Pred. No. 6.3e-78;  
Matches 406; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 130 TATGGCTAGACCAAGCGCTATGACAGCTCTGAAAGTGATGGCGCTATGCGGCC 189  
Db 420 TATGGCTAGACCAAGCGCTATGACAGCTCTGAAAGTGATGGCGGCC 361  
QY 190 GAGCAGTTCAGTGAAGTGGACCAAGCAACCTCAAGAGGGGACAGCAACTCAA 249  
Db 360 GAGCAGTTCAGTGAAGTGGACCAAGCAACCTCAAGAGGGGACAGCAACTCAA 301  
QY 250 CGTCAGGATCCTGAGTGTCTCAGGAGGGAGAGGATGAGGAGCATCTGAGGTCAGGG 309  
Db 300 CGTCAGGATCCTGAGTGTCTCAGGAGGGAGAGGATGAGGAGCATCTGAGGTCAGGG 241  
QY 310 CCGAGCCTGAAGTGTATGATCCAGGACAGGCTCACCCACAGCTGGGTGAGTGTGA 369  
Db 240 CCGAGCCTGAAGTGTATGATCCAGGACAGGCTCACCCACAGCTGGGTGAGTGTGA 181  
QY 370 GATGGTCTGATGGCGCAGGAGATGGACCGCCAAATCCAGAGGAGTGAACCGCTGAA 429  
Db 180 GATGGTCTGATGGCGCAGGAGATGGACCGCCAAATCCAGAGGAGTGAACCGCTGAA 121  
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QY 490 TATGTCGAAATTTGTCATTAATTTCTCCCAATAAGCTTACAGCTTCTCAAGA 549  
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LOCUS K-EST0159805 L8SCK0 Homo sapiens cdna clone L8SCK0-8-B09 5', mRNA  
DEFINITION K-EST0159805 L8SCK0 Homo sapiens cdna clone L8SCK0-8-B09 5', mRNA  
sequence.  
ACCESSION CB115693  
VERSION CB115693.1 GI:27941500  
KEYWORDS EST  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 505)  
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 8 row: B column: 09  
High quality sequence stop: 505.  
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FEATURES  
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ORIGIN  
Query Match 66.8%; Score 374; DB 14; Length 505;  
Best Local Similarity 97.4%; Pred. No. 2e-72;  
Matches 380; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAACTGA 172  
Db 81 GAGGAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAATGA 140  
QY 173 TTGGGCTTATGCGGCCCGAGCAGTTCTAGTGTATGAGTGGAAACAGCAACCTGGAAGAAG 232  
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Db 201 GGGAAACAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGGAGAGATGAGGGAG 260  
QY 293 CATCTGCAGGTCAAGGGCCGGAAGCCTGAAGCTGATAGCCAGGAAACAGGGTCAACCAAGA 352  
Db 261 CATCTGCAGGTCAAGGGCCGGAAGCCTGAAGCTGATAGCCAGGAAACAGGGTCAACCAAGA 320  
QY 353 CTGGGTGTAGTGTGAAGATGGTCTGATGGGAGGAGATGGACCCGCAATCCAGAGG 412  
Db 321 CTGGGTGTAGTGTGAAGATGGTCTGATGGGAGGAGATGGACCCGCAATCCAGAGG 380  
QY 413 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTAAAGAGGACAGCTTGAA 472  
Db 381 AGGTGAAACCGCTGAAAGAGGTGAAAGCAATCACAGTGTAAAGAGGACAGCTTGAA 440  
QY 473 ATGATGAGGCTGCTCCTCTATGTTGAAAT 502  
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Job time : 2818 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2004, 12:43:29 ; Search time 374 Seconds

(without alignments)  
6360.938 Million cell updates/sec

Title: US-09-782-745-15

Perfect score: 560

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5090240

Minimum DB seq length: 0

Maximum DB seq length: 560

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002s:\*

7: geneseqn2003as:\*

8: geneseqn2003bs:\*

9: geneseqn2003cs:\*

10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560	100.0	560	2	AAX90520 GAGE-3 tu
2	552	98.6	560	2	Aav18718 cdna enco
3	446.4	79.7	532	2	Aax90522 GAGE-5 tu
4	443.2	79.1	526	7	ADAI15802 Human GAG
5	443.2	79.1	540	2	Aax90521 GAGE-4 tu
6	441.6	78.9	540	2	AAX90523 GAGE-6 tu
7	438.4	78.3	532	2	Aav18720 cdna enco
8	432	77.1	539	2	Aav18721 cdna enco
9	431.8	77.1	528	6	ABL66323 Lung canc
10	430.8	76.9	528	7	ADAI15801 Human GAG
11	430.2	76.8	527	7	ACC51027 Human bla
12	430.2	76.8	527	7	Abx76236 Lung canc
13	429.2	76.6	538	2	AAX90519 GAGE-2 tu
14	425.8	76.0	541	2	Aav18719 cdna enco
15	421.2	75.2	530	7	ABZ20463 GAGE-2 fu
16	417.6	74.6	535	2	Aav18717 cdna enco
17	304.6	54.4	530	4	AAS60104 Human can
18	302.4	54.0	365	4	AAS60496 Human can
19	265.2	47.4	430	3	AAC02129 Human sec
20	172.2	30.8	520	7	ABT15737 Human can
21	164.6	29.4	509	7	Abx77605 Different
22	164.6	29.4	509	8	ACd42232 Human GAG
23	164.6	29.4	509	9	Adc24646 Human CDN

24	155.4	27.8	503	5	AAS69484	DNA enco
C 25	151.4	27.0	229	7	ABZ18686	Group III
C 26	151.4	27.0	277	7	ABZ19551	Group III
27	149.8	26.8	229	7	ABZ20497	TPS1 subt
C 28	149.8	26.8	257	7	ABZ19955	Group III
29	149.8	26.8	264	7	ABZ19755	Group III
C 30	149.4	26.7	227	7	ABZ20480	Group III
31	147.4	26.3	532	4	AAI60530	Human pol
32	137.4	24.5	225	7	ABZ19533	Group III
33	137.4	24.5	259	7	ABZ19791	Group III
34	132.2	23.6	528	7	ABT15728	Human can
35	128.8	23.0	475	4	AAI14981	Human can
36	123.8	22.1	538	7	ABT15736	Human can
37	108	19.3	399	5	AAF68151	Human can
38	108	19.3	399	6	ABK38062	cdna enco
39	108	19.3	399	7	ACA10391	Human lun
40	108	19.3	399	7	ABX99342	Lung canc
41	108	19.3	399	10	ADE72125	Human lun
42	103.6	18.5	505	6	AAD24228	Human dif
43	103.4	18.5	463	6	ABA92217	Melanoma
44	101.6	18.1	515	4	AAH93807	Human pro
45	101.6	18.1	515	4	AAS63900	Human pro

## ALIGNMENTS

### RESULT 1

AAX90520

ID AAX90520 standard; cdna; 560 BP.

AC AAX90520;

DT 30-SEP-1999 (first entry)

GAGE-3 tumour rejection antigen clone nucleotide sequence.

Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;

OS Homo sapiens.

PN WC9937665-A1.

XX 29-JUL-1999.

PF 12-JAN-1999; 99WO-US000775.

PR 23-JAN-1998; 98US-00012818.

XX (LUDW-) LUDWIG INST CANCER RES.

PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;

XX WPI; 1999-469111/39.

PT New isolated peptides which bind to HLA-A29 molecules, which are tumor rejection antigens used for detection and therapy of pathological conditions, e.g. cancer.

XX Example 13; Fig 4; 62pp; English.

CC The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present invention

XX Sequence 560 BP; 177 A; 119 C; 150 G; 114 T; 0 U; 0 Other;

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Best Local Similarity 100.0%; Pred. No. 4e-151;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||
Qy 1 CTCATATTTTCACACAGATGAGTTGGGAGGAAGATCGACCTATTATTGGTCTAGGCCAAT 60
Db |||

Qy 61 AATAGGTCGATCTTCTCGCCAACTCATATTTTCACACAGATGATCTCAGTAGGAAAA 120
Db |||
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Db |||

Qy 121 TCGACCTATTATTGGGCTAGCAACAGCGCTATGTACAGCTCTCTGAAGTGAATGGGCT 180
Db |||
Qy 121 TCGACCTATTATTGGGCTAGCAACAGCGCTATGTACAGCTCTCTGAAGTGAATGGGCT 180
Db |||

Qy 181 ATGGGCGCCGAGCAGTTTCAGTGTGAATGGAACCCAGCAACACCTGGAAGGGGAACCA 240
Db |||
Qy 181 ATGGGCGCCGAGCAGTTTCAGTGTGAATGGAACCCAGCAACACCTGGAAGGGGAACCA 240
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Qy 241 GCAACTCAACGTCAGGATCTCTGCACTGCTCAGGAGGAGGATGAGGAGCATCTGCA 300
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Qy 301 GGTCAAGGGCGGAGCGCTGAAGCTGATGAGCCAGGAACAGGGTCAACCCACAGACTGGGT 360
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Qy 301 GGTCAAGGGCGGAGCGCTGAAGCTGATGAGCCAGGAACAGGGTCAACCCACAGACTGGGT 360
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Qy 361 GAGTGTGAAGATGCTCTGATGGCGAGGATGACCGCGCAATCCAGAGGAGGTGAAA 420
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Qy 421 ACGCTCGAAGAGGTGAAAACCAATCATCAGTGTAAAGAGGACGCTTGAATGATGCA 480
Db |||
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Qy 481 GGCTGCTCTATGTTGGAAATTTCTTCAATTAATTTCTCCCAATAAAGCTTTACAGCCTT 540
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Qy 541 CTGCAAGAAAAA 560
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Db |||

RESULT 2
AAV18718
ID AAV18718 standard; cDNA; 560 BP.
XX AC AAV18718;
XX 30-JUL-1998 (first entry)
XX DE cDNA encoding GAGE-3 tumour rejection antigen precursor.
XX KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;
XX KW melanoma; antigen; cytolytic T cell clone proliferation;
XX KW HLA-typing assay; ss.
XX OS Homo sapiens.
XX FH Location/Qualifiers
XX FT 100. .457
XX FT /*tag= a
XX FT /transl_except= (pos:217. .219, aa:Ala)
XX FT /transl_except= (pos:220. .222, aa:Thr)
XX PN WO9749417-A1.
XX PD 31-DEC-1997.
XX 23-JUN-1997; 97WO-US010850.
XX PF
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```
XX 24-JUN-1996; 96US-00669161.
XX PR (LUDW-) LUDWIG INST CANCER RES.
XX PA Debacker O, Van Den Eynde B, Boon-Falleur T;
XX PI WPI; 1998-076905/07.
XX DR P-PSDB; AAW47600.
XX DR
XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -
XX processed by HLA-Cw6 molecules into peptides, useful to diagnose
XX melanomas.
XX Example 13; Fig 4; 60pp; English.
XX PS
XX The present sequence encodes a GAGE-3 tumour rejection antigen
XX precursor (TRAP). The protein is expressed in a number of tumours. In
XX contrast the only normal tissue which expresses GAGE TRAP protein is
XX testis. Several GAGE TRAPs have been identified (see AAV18717-21). The
XX major difference between these proteins and GAGE-1 (AAV05540) is the
XX absence of a stretch of 143 bases located at position 379 to 521 of the
XX GAGE-1 TRAP sequence. The rest of the sequences show mismatches at
XX various positions, with the exception of GAGE-3 whose 5' end is totally
XX different from the other GAGE cDNAs for the first 112 bases. This region
XX of GAGE-3 cDNA contains a long repeat and a hairpin structure. The
XX antigens can be used to diagnose melanomas, characterised by expression
XX of a TRAP or presentation of a tumour rejection antigen. Antigens shed
XX into blood or urine can be observed and then used to confirm a diagnosis
XX of melanoma using cytolytic T cell clone proliferation methodologies.
XX Other uses for the processed peptides, include HLA-typing assays for,
XX e.g. skin graft or organ transplants
XX SQ Sequence 560 BP; 175 A; 119 C; 152 G; 114 T; 0 U; 0 Other;
XX
XX Query Match 98.6%; Score 552; DB 2; Length 560;
XX Best Local Similarity 99.1%; Pred. No. 8.1e-149;
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Qy 121 TCGACCTATTATTGGGCTAGCAACAGCGCTATGTACAGCTCTCTGAAGTGAATGGGCT 180
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Qy 121 TCGACCTATTATTGGGCTAGCAACAGCGCTATGTACAGCTCTCTGAAGTGAATGGGCT 180
Db |||

Qy 181 ATGGGCGCCGAGCAGTTTCAGTGTGAATGGAACCCAGCAACACCTGGAAGGGGAACCA 240
Db |||
Qy 181 ATGGGCGCCGAGCAGTTTCAGTGTGAATGGAACCCAGCAACACCTGGAAGGGGAACCA 240
Db |||

Qy 241 GCAACTCAACGTCAGGATCTCTGCACTGCTCAGGAGGAGGATGAGGAGCATCTGCA 300
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Db |||

Qy 301 GGTCAAGGGCGGAGCGCTGAAGCTGATGAGCCAGGAACAGGGTCAACCCACAGACTGGGT 360
Db |||
Qy 301 GGTCAAGGGCGGAGCGCTGAAGCTGATGAGCCAGGAACAGGGTCAACCCACAGACTGGGT 360
Db |||

Qy 361 GAGTGTGAAGATGCTCTGATGGCGAGGATGACCGCGCAATCCAGAGGAGGTGAAA 420
Db |||
Qy 361 GAGTGTGAAGATGCTCTGATGGCGAGGATGACCGCGCAATCCAGAGGAGGTGAAA 420
Db |||

Qy 421 ACGCTCGAAGAGGTGAAAACCAATCATCAGTGTAAAGAGGACGCTTGAATGATGCA 480
Db |||
Qy 421 ACGCTCGAAGAGGTGAAAACCAATCATCAGTGTAAAGAGGACGCTTGAATGATGCA 480
Db |||

Qy 481 GGCTGCTCTATGTTGGAAATTTCTTCAATTAATTTCTCCCAATAAAGCTTTACAGCCTT 540
Db |||
Qy 481 GGCTGCTCTATGTTGGAAATTTCTTCAATTAATTTCTCCCAATAAAGCTTTACAGCCTT 540
Db |||
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Db 481 GGCTGCTCTATGTTGGAAATTTGTTCAATTAATAATCTCCCAATAAAGCTTTTACAGCCTT 540

QY 541 CTGCAAGAGAAAAA 560

Db 541 CTGCAAGAGAAAAA 560

RESULT 3

AAAX90522

ID AAX90522 standard; cDNA; 532 BP.

XX AAX90522;

XX 30-SEP-1999 (first entry)

DE GAGE-5 tumour rejection antigen clone nucleotide sequence.

XX Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;

KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;

KW GAGE; ss.

XX Homo sapiens.

XX NC09937665-A1.

XX 29-JUL-1999.

XX 12-JAN-1999; 99WO-US000775.

XX 23-JAN-1998; 98US-00012818.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;

PI WPI; 1999-469111/39.

XX New isolated peptides which bind to HLA-A29 molecules, which are tumor

PT rejection antigens used for detection and therapy of pathological

PT conditions, e.g. cancer.

XX Example 13; Fig 4; 62pp; English.

XX The present invention describes peptides which bind to human leukocyte

CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into

CC tumour rejection antigens. They can be used for detecting cytolytic T

CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-

CC typing assays. Complexes of HLA-29 molecules and the peptides can be used

CC for stimulating CTLs in vivo. The present sequence represents a GAGE

CC tumour rejection antigen clone, from an example from the present

CC invention

XX Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 U; 0 Other;

SQ

Query Match 79.7%; Score 446.4; DB 2; Length 532;

Best Local Similarity 99.8%; Pred. No. 2.3e-118;

Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 85 GAGGAAGATCGACCTATTATTGGCTAGACCAAGGCGTATGTACAGCCTCTGAGTGA 144

QY 173 TTGGGCTATGGCCGAGCAGTTCAGTGAAGTGAACCAACCTGAGAG 232

Db 145 TTGGGCTATGGCCGAGCAGTTCAGTGAAGTGAACCAACCTGAGAG 204

QY 233 GGGAAACCACTCAACCTCAGGATCTCTGAGCTGCTCAGGAGGAGAGGATGAGGAG 292

Db 205 GGGAAACCACTCAACCTCAGGATCTCTGAGCTGCTCAGGAGGAGAGGATGAGGAG 264

QY 293 CATCTGCAGTCAAGGCCGAGCCTGAGTGTAGCCAGAAACAGGCTACCCACAGA 352

Db 265 CATCTGCAGTCAAGGCCGAGCCTGAGTGTAGCCAGAAACAGGCTACCCACAGA 324

QY 353 CTGGGTGTGAGTGTGAAGATGGTCTGTATGGGCGAGAGATGGACCGCCAAATCCAGAGG 412

Db 325 CTGGGTGTGAGTGTGAAGATGGTCTGTATGGGCGAGAGATGGACCGCCAAATCCAGAGG 384

QY 413 AGGTGAAAACGCTGAGAGAGGTGAAAAGCAATCAGAGTGTAAAGAGGCGAGCTTGAA 472

Db 385 AGGTGAAAACGCTGAGAGAGGTGAAAAGCAATCAGAGTGTAAAGAGGCGAGCTTGAA 444

QY 473 ATGATCAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATAATCTCCCAATAAAGCTTT 532

Db 445 ATGATCAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATAATCTCCCAATAAAGCTTT 504

QY 533 ACAGCCTTCTGCAAGAAAAA 560

Db 505 ACAGCCTTCTGCAAGAAAAA 532

## RESULT 4

ADAI5802

ID ADAI5802 standard; cDNA; 526 BP.

XX ADAI5802;

XX 06-NOV-2003 (first entry)

XX Human GAGE-7B cDNA.

XX Human; GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL;

KW human leukocyte antigen; HLA; tumour rejection antigen precursor;

KW major histocompatibility complex; MHC; cytolytic T cell proliferation;

KW chromosome Xp11.2-p11.4.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX 55..408

XX /\*tag= a

XX /product= "Human GAGE-7B"

XX /transl\_except= {pos:115..162, aa: GPMRPEQSGDVEPEM}

XX /transl\_except= {pos:265..306, aa: HPQTGKPEAHSQBQ}

XX US6509172-B1.

XX 21-JAN-2003.

XX 30-SEP-1998; 98US-00163748.

XX 30-SEP-1998; 98US-00163748.

XX (LUDW-) LUDWIG INST CANCER RES.

XX De Backer O, Van Den Eynde B, Boon-Falleur T;

XX WPI; 2003-401119/38.

XX P-PSDB; ADAI5777.

XX New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor

PT rejection antigen precursors, which complex to major histocompatibility

PT complex molecules to facilitate the proliferation of cytolytic T cells.

XX Claim 1; Col 9-10; 15pp; English.

XX The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the

CC nucleic acid molecules encoding them. The invention also relates to an

CC expression vector comprising an isolated nucleic acid molecule of the

CC invention operably linked to a promoter, a recombinant cell comprising

CC the isolated nucleic acid molecule or the expression vector and an

CC expression kit useful in generating cytolytic T lymphocytes (CTLs) or

CC determining if CTLs are present in a sample comprising the isolated

CC nucleic acid molecule and the isolated nucleic acid that encodes a human

CC leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid

CC molecules encode tumour rejection antigen precursors, which complex to

CC major histocompatibility complex (MHC) molecules to facilitate the  
CC proliferation of cytolytic T cells. This sequence represents cDNA  
CC encoding the human GAGE-7B polypeptide of the invention. The gene resides  
CC on chromosome Xp11.2-p11.4.

XX  
SQ Sequence 526 BP; 168 A; 109 C; 143 G; 106 T; 0 U; 0 Other;

Query Match 79.1%; Score 443.2; DB 7; Length 526;  
Best Local Similarity 99.3%; Pred. No. 1.9e-117;  
Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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DB 65 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 124  
QY 173 TTGGGCTTATGCGGCCGAGAGTTTCAGTGTGATGAAGTGGAAACCAAGCAACCTGAAGAAG 232  
DB 125 TTGGGCTTATGCGGCCGAGAGTTTCAGTGTGATGAAGTGGAAACCAAGCAACCTGAAGAAG 184  
QY 233 GGGAAACAGCAACTCAACGTCAGGATCTGCGAGTGTCTCAGGAGGGAGAGGATCAGGAG 292  
DB 185 GGGAAACAGCAACTCAACGTCAGGATCTGCGAGTGTCTCAGGAGGGAGAGGATCAGGAG 244  
QY 293 CATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGTAGCTGTAGCCAGGAACAGGGTCAACCAAGA 352  
DB 245 CATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGTAGCCAGGAACAGGGTCAACCAAGA 304  
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DB 305 CTGGGTGTGAGTGTGAAGATGGTCTGTATGGGAGGAGATGGACCCGCAATCAAGCTT 364  
QY 413 AGGTGAAACCGCTGAAGAGGTGAAAGCAATCACAGTGTAAAGAGAGGACAGTTGAA 472  
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QY 473 ATGATGAGGCTGTCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532  
DB 425 ATGATGAGGCTGTCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 484  
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DB 485 ACAGCTTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 512

## RESULT 5

AAAX90521  
ID AAAX90521 standard; cDNA; 540 BP.

XX  
AC AAAX90521;

XX  
DT 30-SEP-1999 (first entry)

XX  
DE GAGE-4 tumour rejection antigen clone nucleotide sequence.

XX  
KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
KW GAGE; ss.

XX  
OS Homo sapiens.

XX  
PN WO9937665-A1.

XX  
PD 29-JUL-1999.

XX  
PF 12-JAN-1999; 99WO-US000775.

XX  
PR 23-JAN-1998; 98US-00012818.

XX  
PA (LUDWIG) LUDWIG INST CANCER RES.

XX  
PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Palleur T;

XX  
DR WPI; 1999-469111/39.

XX

PT New isolated peptides which bind to HLA-A29 molecules, which are tumor  
PT rejection antigens used for detection and therapy of pathological  
PT conditions, e.g. cancer.

XX  
PS Example 13; Fig 4; 62pp; English.

XX  
CC The present invention describes peptides which bind to human leukocyte  
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into  
CC tumour rejection antigens. They can be used for detecting cytolytic T  
CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-  
CC typing assays. Complexes of HLA-29 molecules and the peptides can be used  
CC for stimulating CTLs in vivo. The present sequence represents a GAGE  
CC tumour rejection antigen clone, from an example from the present  
CC invention

XX  
SQ Sequence 540 BP; 159 A; 114 C; 156 G; 111 T; 0 U; 0 Other;

Query Match 79.1%; Score 443.2; DB 2; Length 540;  
Best Local Similarity 99.3%; Pred. No. 1.9e-117;  
Matches 445; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172  
DB 93 GAGGAAATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 152  
QY 173 TTGGGCTTATGCGGCCGAGAGTTTCAGTGTGATGAAGTGGAAACCAAGCAACCTGAAGAAG 232  
DB 153 TTGGGCTTATGCGGCCGAGAGTTTCAGTGTGATGAAGTGGAAACCAAGCAACCTGAAGAAG 212  
QY 233 GGGAAACAGCAACTCAACGTCAGGATCTGCGAGTGTCTCAGGAGGGAGAGGATCAGGAG 292  
DB 213 GGGAAACAGCAACTCAACGTCAGGATCTGCGAGTGTCTCAGGAGGGAGAGGATCAGGAG 272  
QY 293 CATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGTAGCCAGGAACAGGGTCAACCAAGA 352  
DB 273 CATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGTAGCCAGGAACAGGGTCAACCAAGA 332  
QY 353 CTGGGTGTGAGTGTGAAGATGGTCTGTATGGGAGGAGATGGACCCGCAATCAAGCTT 412  
DB 333 CTGGGTGTGAGTGTGAAGATGGTCTGTATGGGAGGAGATGGACCCGCAATCAAGCTT 392  
QY 413 AGGTGAAACCGCTGAAGAGGTGAAAGCAATCACAGTGTAAAGAGAGGACAGTTGAA 472  
DB 393 AGGTGAAACCGCTGAAGAGGTGAAAGCAATCACAGTGTAAAGAGAGGACAGTTGAA 452  
QY 473 ATGATGAGGCTGTCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532  
DB 453 ATGATGAGGCTGTCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 512  
QY 533 ACAGCTTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 560  
DB 513 ACAGCTTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

## RESULT 6

AAAX90523

ID AAAX90523 standard; cDNA; 540 BP.

XX  
AC AAAX90523;

XX  
DT 30-SEP-1999 (first entry)

XX  
DE GAGE-6 tumour rejection antigen clone nucleotide sequence.

XX  
KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
KW GAGE; ss.

XX  
OS Homo sapiens.

XX  
PN WO9937665-A1.

XX



Db 265 CATCTGAGTCAAGGCCGAGCCTGAAGCTGATAGCCAGGACACAGGTCACCCACAGA 324

QY 353 CTGGGTGTAGTGTGAAGATGTCCTGATGGGAGGAGATGGACCCGCCAAATCCAGAGG 412

Db 325 CTGGGTGTAGTGTGAAGATGTCCTGATGGGAGGAGATGGACCCGCCAAATCCAGAGG 384

QY 413 AGGTGAAGACGCTGAGAGAGGTGAAGCAATCACAGTCTTAAAGAGGCGTGTGAA 472

Db 385 AGGTGAAGACGCTGAGAGAGGTGAAGCAATCACAGTCTTAAAGAGGCGTGTGAA 444

QY 473 ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532

Db 445 ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 504

QY 533 ACAGCCTTCTGCAAGAAAAA 560

Db 505 ACAGCCTTCTGCAAGAAAAA 532

RESULT 8

AAV18721

ID AAV18721 standard; cDNA; 539 BP.

XX

AC AAV18721;

XX

DT 30-JUL-1998 (first entry)

XX

DE cDNA encoding GAGE-6 tumour rejection antigen precursor.

XX

KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;

KW melanoma; antigen; cytolytic T cell clone proliferation;

KW HLA-typing assay; ss.

XX

OS Homo sapiens.

XX

FH Key

CD5 Location/Qualifiers

82..436

/\*tag= a

/transl\_except= (pos:127..129, aa:Arg)

/transl\_except= (pos:196..198, aa:Ala)

/transl\_except= (pos:199..201, aa:Thr)

XX

FN W09749417-A1.

XX

PD 31-DEC-1997.

XX

PF 23-JUN-1997; 97WO-US010850.

XX

PR 24-JUN-1996; 96US-00669161.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Debacker O, Van Den Eynde B, Boon-Falleur T;

XX

DR WPI; 1998-076905/07.

XX

DR P-PSDB; AAW47603.

XX

PT Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -

PT processed by HLA-Cw6 molecules into peptides, useful to diagnose

PT melanomas.

XX

PS Example 13; Fig 4; 60pp; English.

XX

CC The present sequence encodes a GAGE-6 tumour tumour rejection antigen

CC precursor (TRAP). The protein is expressed in a number of tumours. In

CC contrast the only normal tissue which expresses GAGE TRAP protein is

CC testis. Several GAGE TRAPs have been identified (see AAV18717-21). The

CC major difference between these proteins and GAGE-1 (AAV05540) is the

CC absence of a stretch of 143 bases located at position 379 to 521 of the

CC GAGE-1 TRAP sequence. The rest of the sequences show mismatches at

CC various position, with the exception of GAGE-3 whose 5' end is totally

CC different from the other GAGE cDNAs for the first 112 bases. This region

CC of GAGE-3 cDNA contains a long repeat and a hairpin structure. The

CC antigens can be used to diagnose melanomas, characterised by expression

CC of a TRAP or presentation of a tumour rejection antigen. Antigens shed

CC into blood or urine can be observed and then used to confirm a diagnosis

CC of melanoma using cytolytic T cell clone proliferation methodologies.

CC Other uses for the processed peptides, include HLA-typing assays for,

CC e.g. skin graft or organ transplants

XX Sequence 539 BP; 157 A; 114 C; 157 G; 111 T; 0 U; 0 Other;

QY Query Match 77.1%; Score 432; DB 2; Length 539;

Best Local Similarity 97.8%; Pred. No. 3.3e-114;

Matches 438; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 113 GAGGAAATCGACCTATTATTGGCTAGACCAAGGCGCTATGTACAGCTCTCTGAAGTGA 172

Db 92 GAGGAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGTACAGCTCTCTGAAGTGA 151

QY 173 TTGGGCTATGCGGCCGAGCAGTTTCAGTGAATGGAACGACCAACCTCTGAAGAAG 232

Db 152 TTGGGCTATGCGGCCGAGCAGTTTCAGTGAATGGAACGACCAACCTCTCTGAAGAAG 211

QY 233 GGGNACCAGCACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGAGATCAGGAG 292

Db 212 GGGNACCAGCACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGAGATCAGGAG 271

QY 293 CATCTGAGTCAAGGGCCGAGCCTGAAGCTGATAGCCAGGACACAGGTCACCCACAGA 352

Db 272 CATCTGAGTCAAGGGCCGAGCCTGAAGCTGATAGCCAGGACACAGGTCACCCACAGA 331

QY 353 CTGGGTGTAGTGTGAAGATGTCCTGATGGGAGGAGATGGACCCGCCAAATCCAGAGG 412

Db 332 CTGGGTGTAGTGTGAAGATGTCCTGATGGGAGGAGATGGACCCGCCAAATCCAGAGG 391

QY 413 AGGTGAAGACGCTGAGAGAGGTGAAGCAATCACAGTGTAAAGAGGCGTGTGAA 472

Db 392 AGGTGAAGACGCTGAGAGAGGTGAAGCAATCACAGTGTAAAGAGGCGTGTGAA 451

QY 473 ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 532

Db 452 ATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATTTCTCCCAATAAGCTTT 511

QY 533 ACAGCCTTCTGCAAGAAAAA 560

Db 512 ACAGCCTTCTGCAAGAAAAA 539

## RESULT 9

ABL66323

ID ABL66323 standard; DNA; 528 BP.

XX ABL66323;

DT 15-MAY-2002 (first entry)

XX Lung cancer related gene sequence SEQ ID NO:4660.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

XX cycstatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

XX gene; ds.

OS Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US010838.

XX 05-JUN-2000; 2000US-0209473P.

XX 05-JUN-2000; 2000US-0209531P.

XX 18-SEP-2000; 2000US-0233133P.

XX 18-SEP-2000; 2000US-0233617P.



PR 20-SEP-2000; 2000US-0234009P.  
 PR 20-SEP-2000; 2000US-0234034P.  
 PR 20-SEP-2000; 2000US-0234052P.  
 PR 22-SEP-2000; 2000US-0234509P.  
 PR 22-SEP-2000; 2000US-0234567P.  
 PR 25-SEP-2000; 2000US-0234923P.  
 PR 25-SEP-2000; 2000US-0234924P.  
 PR 25-SEP-2000; 2000US-0235077P.  
 PR 25-SEP-2000; 2000US-0235082P.  
 PR 25-SEP-2000; 2000US-0235134P.  
 PR 25-SEP-2000; 2000US-0235280P.  
 PR 26-SEP-2000; 2000US-0235637P.  
 PR 26-SEP-2000; 2000US-0235638P.  
 PR 27-SEP-2000; 2000US-0235711P.  
 PR 27-SEP-2000; 2000US-0235720P.  
 PR 27-SEP-2000; 2000US-0235840P.  
 PR 27-SEP-2000; 2000US-0235840P.  
 PR 28-SEP-2000; 2000US-0235863P.  
 PR 28-SEP-2000; 2000US-0236028P.  
 PR 28-SEP-2000; 2000US-0236032P.  
 PR 28-SEP-2000; 2000US-0236033P.  
 PR 28-SEP-2000; 2000US-0236034P.  
 PR 28-SEP-2000; 2000US-0236109P.  
 PR 28-SEP-2000; 2000US-0236111P.  
 PR 29-SEP-2000; 2000US-0236842P.  
 PR 29-SEP-2000; 2000US-0236891P.  
 PR 02-OCT-2000; 2000US-0237172P.  
 PR 02-OCT-2000; 2000US-0237173P.  
 PR 02-OCT-2000; 2000US-0237278P.  
 PR 02-OCT-2000; 2000US-0237294P.  
 PR 02-OCT-2000; 2000US-0237295P.  
 PR 03-OCT-2000; 2000US-0237316P.  
 PR 03-OCT-2000; 2000US-0237425P.  
 PR 03-OCT-2000; 2000US-0237598P.  
 PR 03-OCT-2000; 2000US-0237604P.  
 PR 03-OCT-2000; 2000US-0237606P.  
 PR 03-OCT-2000; 2000US-0237608P.  
 PR 01-NOV-2000; 2000US-0244867P.  
 PR 01-NOV-2000; 2000US-0245084P.  
 PA (AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 PI Soppet DR, Weaver Z;  
 PI WPI; 2002-188264/24.

PT Screening for anti-neoplastic agent involves exposing cells to a chemical  
 PT agent to be tested for anti-neoplastic activity, and determining a change  
 PT in expression of a gene of a signature gene set.

XX Claim 1; SEQ ID NO 4660; 44pp; English.

CC The present invention describes a method (M1) for screening for an anti-  
 CC neoplastic agent. The method involves exposing cells to a chemical agent  
 CC to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in AB161664  
 CC to AB170110), or is at least 95% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening an  
 CC anti-neoplastic agent, and can be used for producing a product which is  
 CC the data collected with respect to the anti-neoplastic agent as a result  
 CC of M1, and the data is sufficient to convey the chemical structure and/or  
 CC properties of the agent. M1 can be used in the treatment of cancer such  
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms  
 CC tumour

XX Sequence 528 BP; 147 A; 114 C; 156 G; 111 T; 0 U; 0 Other;

XX Query Match 77.1%; Score 431.8; DB 6; Length 528;

Best Local Similarity 99.5%; Pred. No. 3.7e-114;  
 Matches 433; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 113 GAGGAAATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGACAGCCCTCCTGAAGTGA 172  
 DB |||||  
 QY 93 GAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGACAGCCCTCCTGAAGTGA 152  
 DB |||||  
 QY 173 TTGGGCTATGCGGCCCGAGCGTTCAGTGAGTGAAGCAACAGCAACACCTGAAGAAG 232  
 DB |||||  
 QY 153 TTGGGCTATGCGGCCCGAGCGTTCAGTGAGTGAAGCAACAGCAACACCTGAAGAAG 212  
 DB |||||  
 QY 233 GGGACCCAGCAACTCAACCTCAGGATCCTGCGAGCTCTCAGGAGGAGAGGATCAGGGAG 292  
 DB |||||  
 QY 213 GGGACCCAGCAACTCAACCTCAGGATCCTGCGAGCTCTCAGGAGGAGAGGATCAGGGAG 272  
 DB |||||  
 QY 293 CATCTGAGGTCAAGGGCGCGAAGCCTGAAGCTGATAGCCAGCAACAGGCTCACCCACAGA 352  
 DB |||||  
 QY 273 CATCTGAGGTCAAGGGCGCGAAGCCTGAAGCTGATAGCCAGCAACAGGCTCACCCACAGA 332  
 DB |||||  
 QY 353 CTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGACCCGCCAAATCCAGAGG 412  
 DB |||||  
 QY 333 CTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGACCCGCCAAATCCAGAGG 392  
 DB |||||  
 QY 413 AGGTGAAAACGCGCTGAAGAAGGTGAAGAAGCAATCAGTGTAAAGAGGACAGCTTGA 472  
 DB |||||  
 QY 393 AGGTGAAAACGCGCTGAAGAAGGTGAAGAAGCAATCAGTGTAAAGAGGACAGCTTGA 452  
 DB |||||  
 QY 473 ATGATGAGGCTGCTCCTATGTTGGAAATTTCTTCATTAATAATTTCCCAATAGCTTT 532  
 DB |||||  
 QY 453 ATGATGAGGCTGCTCCTATGTTGGAAATTTCTTCATTAATAATTTCCCAATAGCTTT 512  
 DB |||||  
 QY 533 ACAGCCTTCTGCAAA 547  
 DB |||||  
 QY 513 ACAGCCTTCTGCAAA 527  
 DB |||||

## RESULT 10

ADAL5801  
 ID ADAL5801 standard; cDNA; 528 BP.

XX ADAL5801;

XX 06-NOV-2003 (first entry)

XX Human GAGE-8 cDNA.

XX Human; GAGE-8; Gene; ss; cytolytic T lymphocyte; CTL;  
 KW human leukocyte antigen; HLA; tumour rejection antigen precursor;  
 KW major histocompatibility complex; MHC; cytolytic T cell proliferation;  
 KW Chromosome Xp11.2-p11.4.

XX Homo sapiens.

XX Key Location/Qualifiers  
 XX CDS 73..423

FT /\*tag= a  
 FT /product= "Human GAGE-8"  
 FT /transl\_except= (pos:244..246, aa:Gln)  
 FT /transl\_except= (pos:400..402, aa:Lys)

XX US6509172-B1.

XX 21-JAN-2003.

XX 30-SEP-1998; 98US-00163748.

XX 30-SEP-1998; 98US-00163748.

XX (LUDW-) LUDWIG INST CANCER RES.

XX De Backer O, Van Den Eynde B, Boon-Falleur T;

XX WPI; 2003-401119/38.

DR	P-PSDB; ADA15778..
XX	
PT	New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor
PT	rejection antigen precursors, which complex to major histocompatibility
PT	complex molecules to facilitate the proliferation of cytolytic T cells.
XX	
XX	Claim 1; Col 7-10; 15pp; English.
XX	
CC	The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the
CC	nucleic acid molecules encoding them. The invention also relates to an
CC	expression vector comprising an isolated nucleic acid molecule of the
CC	invention operably linked to a promoter, a recombinant cell comprising
CC	the isolated nucleic acid molecule or the expression vector and an
CC	expression kit useful in generating cytolytic T lymphocytes (CTLs) or
CC	determining if CTLs are present in a sample comprising the isolated
CC	nucleic acid molecule and the isolated nucleic acid that encodes a human
CC	leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid
CC	molecules encode tumour rejection antigen precursors, which complex to
CC	major histocompatibility complex (MHC) molecules to facilitate the
CC	proliferation of cytolytic T cells. This sequence represents cDNA
CC	encoding the human GAGE-8 polypeptide of the invention. The gene resides
CC	on chromosome Xp11.2-p11.4.
CC	
XX	Sequence 528 BP; 158 A; 112 C; 151 G; 107 T; 0 U; 0 Other;
XX	
SO	

Query Match	76.9%	Score 430.8	DB 7	Length 528
Best Local Similarity	92.4%	Pred. No. 7.1e-114		
Matches 453; Conservative 0;	Mismatches 37;	Indels 0;	Gaps 0;	
QY	71	TCCTCTCGGCAACTCATATTTACACAGATGAATCTCAGTAGAGGAAAAATCGACCTATT	130	
Db	38	TCCTTTTCCCTCTACTGAGATTCATCTGTGTGAATATATGAGTTGGCGAGGAATCGACCT	97	
QY	131	ATTGGGCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGAATTGGGCTTATGGGGCCG	190	
Db	98	ATCGGCTAGACCAAGACGCTACCTAGAGCCTCTGAAATGATTGGGCTATGCGGCCG	157	
QY	191	AGCAGTTCAGTGATGAAGTGGAAACCGAACCACTCGAAGAAAGGGGAACACGACACTCAAC	250	
Db	158	AGCAGTTCAGTGATGAAGTGGAAACCGAACCACTCGAAGAAAGGGGAACACGACACTCAAC	217	
QY	251	GTCCAGATCCTGCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTCAGGTCAAGGGC	310	
Db	218	GTCCAGATCCTGCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTCAGGTCAAGGGC	277	
QY	311	CGAAGGCTGAAGCTGATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAG	370	
Db	278	CGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAG	337	
QY	371	ATGGTCTGTATGGCAGGAGATGAACCGGCCAAATCCAGAGGAGGTGAAAACGCTGAAG	430	
Db	338	ATGGTCTGTATGGCAGGAGATGAACCGGCCAAATCCAGAGGAGGTGAAAACGCTGAAG	397	
QY	431	ARGGTGAAAAGCAATCACAGTGTGTAAAGAGGACCGTTGAATCATCAGGCTGCTCCT	490	
Db	398	AAGGTGAAAAGCAATCACAGTGTGTAAAGAGGACCGTTGAATCATCAGGCTGCTCCT	457	
QY	491	ATGTTGGAAAAATTTGTTCAATTAATAATCTCCCAATAAAGCTTTTACAGCCCTTCTGCAAGAA	550	
Db	458	ATGTTGAAATTTGTTCAATTAATAATCTCCCAATAAAGCTTTTACAGCCCTTCTGCAAGAA	517	
QY	551	AAAAAAAAA 560		
Db	518	AAAAAAAAA 527		

RESULT 11  
ACC51027  
ID ACC51027 standard; cDNA; 527 BP.  
XX  
AC ACC51027;  
XX  
DT 12-JUN-2003 (first entry)

XX Human bladder cancer associated cDNA sequence SEQ ID NO:144.  
XX  
XX Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.  
XX Homo sapiens.  
XX WO2003003906-A2.  
XX  
XX 16-JAN-2003.  
XX  
XX 03-JUL-2002; 2002WO-US021338.  
XX  
XX 03-JUL-2001; 2001US-0302814P.  
XX 03-AUG-2001; 2001US-0310099P.  
XX 08-NOV-2001; 2001US-0343705P.  
XX 13-NOV-2001; 2001US-0350666P.  
XX 12-APR-2002; 2002US-0372246P.  
XX (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
XX Mack DH, Aziz N;  
XX  
XX WPI; 2003-201532/19.  
XX P-PSDB; ABR48213.  
XX  
XX Detecting a bladder cancer-associated transcript in a cell from a  
XX patient, comprises contacting a biological sample from the patient with a  
XX bladder cancer-associated polynucleotide or antibody.  
XX  
XX Claim 6; Page 279; 307pp; English.  
XX  
XX The present invention describes a method for detecting a bladder cancer-  
XX associated transcript in a cell from a patient. The method comprises  
XX contacting a biological sample from the patient with a polynucleotide  
XX that selectively hybridises to a sequence that is 80 % identical to a  
XX table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059  
XX encode the human bladder cancer-associated proteins given in ABR48146 to  
XX ABR48242). Bladder cancer-associated sequences from the present invention  
XX have cytostatic activities, and can be used in antisense gene therapy and  
XX in vaccine production. The method can be used for detecting a bladder  
XX cancer-associated transcript in a cell from a patient. The method is  
XX useful in diagnosing or treating bladder cancer and in screening for  
XX compounds that modulate bladder cancer, such as hormones or antibodies.  
XX The nucleic acid molecules from the present invention may be used in  
XX various screening and diagnostic methods, and for gene therapy, vaccine  
XX and/or antisense/inhibition applications  
XX  
XX Sequence 527 BP: 146 A: 113 C: 157 G: 111 T: 0 U: 0 Other:

Query Match	76.8%	Score 430.2	DB 7	Length 527
Best Local Similarity	99.3%	Pred. No. 1.1e-113		
Matches 432	Conservative 0	Mismatches 13	Indels 0	Gaps 0
QY	113	GAGGAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGA	172	
Db	92	GAGGAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGA	151	
QY	173	TTGGGCCTATCGGGCCGAGCAGTTCACTGATGAGTGGAAACAGACAAACACTCTGAGAG	232	
Db	152	TTGGGCCTATCGGGCCGAGCAGTTCACTGATGAGTGGAAACAGACAAACACTCTGAGAG	211	
QY	233	GGGAACCAAGCAACTCAAGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAG	292	
Db	212	GGGAACCAAGCAACTCAAGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAG	271	
QY	293	CATCTGCAGGTCAAGGCCGAGCCTCAAGCTGATGCCAGAACAGGGGTCACCACAGA	352	
Db	272	CATCTGCAGGTCAAGGCCGAGCCTCAAGCTGATGCCAGAACAGGGGTCACCACAGA	331	
QY	353	CTGGGTGTGAGTGAAGATCGTCTGATGGCCAGGAGATGGACCCGCCAAATCCGAGG	412	
Db	332	CTGGGTGTGAGTGAAGATCGTCTGATGGCCAGGAGTGGACCCGCCAAATCCGAGG	391	

QY 413 AGGTGAAAACGGCTGAAGAGCTGAAAGCAATCACAGTGTAAAGAGGACGTTGAA 472  
 DB 392 AGGTGAAAACGGCTGAAGAGGTTGAAAAGCAATCACAGTGTAAAGAGGACGTTGAA 451  
 QY 473 ATGATGCGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATAATTCCTCCCAATAAGCTTT 532  
 DB 452 ATGATGCGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATAATTCCTCCCAATAAGCTTT 511  
 QY 533 ACAGCCTTCTGCAA 547  
 DB 512 ACAGCCTTCTGCAA 526

## RESULT 12

ABX76236

ID ABX76236 standard; DNA; 527 BP.

AC XX

XX ABX76236;

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polynucleotide #105.

XX Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;  
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX WO200286443-A2.

XX PD 31-OCT-2002.

XX PF 18-APR-2002; 2002WO-US012476.

XX PR 18-APR-2001; 2001US-0284770P.

XX PR 10-MAY-2001; 2001US-0290492P.

XX PR 09-NOV-2001; 2001US-0339245P.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 29-NOV-2001; 2001US-0334370P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Aziz N, Murray R;

XX DR WPI; 2003-093161/08.

XX P-PSDB; ABU56512.

XX Detecting a lung cancer-associated transcript in a cell from a patient  
 for treating lung cancer, by contacting a biological sample from the  
 patient with a polynucleotide that exhibits increased or decreased  
 expression in lung cancer.

XX Claim 22; Page 273; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated  
 transcript in a cell from a patient, comprising contacting a biological  
 sample from the patient with a polynucleotide that selectively hybridises  
 to a sequence that is at least 80 % identical to a gene that exhibits  
 increased or decreased expression in lung cancer samples. Lung cancer-  
 associated polynucleotides and polypeptides are used for identifying a  
 compound that modulates a lung cancer-associated polypeptide, for  
 inhibiting proliferation of a lung cancer-associated cell to treat lung  
 cancer in a patient and for treating a mammal having lung cancer by  
 administering a modulatory compound identified. The methods are useful  
 for treating lung cancer, such as small cell lung cancer, non-small cell  
 lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
 emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
 hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and

CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
 CC for diagnostic purposes and as targets for screening for therapeutic  
 CC compounds that modulate lung cancer, such as antibodies. Sequences  
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the  
 CC invention

SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 76.8%; Score 430.2; DB 7; Length 527;

Matches 432; Conservative 99.3%; Pred. No. 1.1e-113;

Mismatches 3; Indels 0; Gaps 0;

QY 113 GAGGAAAATCGACCTATTATTGGCCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 172

DB 92 GAGGAAAGATCGACCTATTATTGGCCTAGACCAAGCGCTATGTACAGCTCTCTGAAGTGA 151

QY 173 TTGGCCCTATGCGCCCGAGCAGTTCAGTGATGAAAGTGAACCAAGCGCTAGAGAG 232

DB 152 TTGGCCCTATGCGCCCGAGCAGTTCAGTGATGAAAGTGAACCAAGCGCTAGAGAG 211

QY 233 GGGAAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGAGGATGAGGAG 292

DB 212 GGGAAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGAGGATGAGGAG 271

QY 293 CATCTGCAAGTCAAGGCGCGAAGCCTGAAGCTGTAGCCAGGAAACAGGGTCAACCCACAGA 352

DB 272 CATCTGCAAGTCAAGGCGCGAAGCCTGAAGCTGTAGCCAGGAAACAGGGTCAACCCACAGA 331

QY 353 CTGGGTGTGAGTGTGAAGATGCTCTGATGGCGAGGATGACCCGCCAATCCAGAGG 412

DB 332 CTGGGTGTGAGTGTGAAGATGCTCTGATGGCGAGGATGACCCGCCAATCCAGAGG 391

QY 413 AGGTGAAAACGCTGAAGAGGTGAAAAGCAATCACAGTGTAAAGAGGACACGTTGAA 472

DB 392 AGGTGAAAACGCTGAAGAGGTGAAAAGCAATCACAGTGTAAAGAGGACACGTTGAA 451

QY 473 ATGATGCAAGGCTGCTCCTATGTTGGAATTTGTCATTAAATTTCTCCCAATAAGCTTT 532

DB 452 ATGATGCAAGGCTGCTCCTATGTTGGAATTTGTCATTAAATTTCTCCCAATAAGCTTT 511

QY 533 ACAGCCTTCTGCAA 547

DB 512 ACAGCCTTCTGCAA 526

## RESULT 13

AAAX90519

ID AAAX90519 standard; cDNA; 538 BP.

XX AC AAAX90519;

XX DT 30-SEP-1999 (first entry)

XX DE GAGE-2 tumour rejection antigen clone nucleotide sequence.

XX KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;

XX KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;

XX KW GAGE; ss.

XX OS Homo sapiens.

XX FN WO9937665-A1.

XX PD 29-JUL-1999.

XX PF 12-JAN-1999; 99WO-US000775.

XX PR 23-JAN-1998; 98US-00012818.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;

XX XX

```
DR WPI; 1999-469111/39.
XX
PT New isolated peptides which bind to HLA-A29 molecules, which are tumor
PT rejection antigens used for detection and therapy of pathological
PT conditions, e.g. cancer.
XX
XX Example 13; Fig 4; 62pp; English.
XX
CC The present invention describes peptides which bind to human leukocyte
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into
CC tumour rejection antigens. They can be used for detecting cytolytic T
CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-
CC typing assays. Complexes of HLA-29 molecules and the peptides can be used
CC for stimulating CTLs in vivo. The present sequence represents a GAGE
CC tumour rejection antigen clone, from an example from the present
CC invention
XX
SQ Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;
Query Match 76.6%; Score 429.2; DB 2; Length 538;
Best Local Similarity 92.2%; Pred. No. 2.1e-113;
Matches 452; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 71 TCTTCTCGCCAACTCATATTTTCACACAGATGAATCTCAGTAGAGGAAATCGACCTATT 130
Db 49 TCITTTTCTCTACTAGATTTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCT 108
QY 131 ATTGGCCTAGACCAAGCGCTATGTACAGCCTCTGAAAGTATGGCCCTATGGGCCCG 190
Db 109 ATCGGCCCTAGACCAAGACGCTACTAGAGCCTCTCTGAAATGATTTGGGCCCTATGGGCCCG 168
QY 191 AGCAGTTTCAGTGAAGTGAAGCCAGCACACCTGAAGAGGGAACCAAGCACTCAAC 250
Db 169 AGCAGTTTCAGTGAAGTGAAGCCAGCACACCTGAAGAGGGAACCAAGCACTCAAC 228
QY 251 GTCAGGATCTCTGACGTGCTCAGAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGC 310
Db 229 GTCAGGATCTCTGACGTGCTCAGAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGC 288
QY 311 CGAAGCCTGAAGCTGTATGACAGAAACAGGGTCAACACAGACTGGGTGTGAGTGTGAAG 370
Db 289 CGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCAACACAGACTGGGTGTGAGTGTGAAG 348
QY 371 ATGTCCTGTGAGGCGAGAGATGACCGCCAAATCCAGAGAGGTTGAACACGCTCAAG 430
Db 349 ATGTCCTGTGAGGCGAGAGATGACCGCCAAATCCAGAGAGGTTGAACACGCTCAAG 408
QY 431 AAGGTGAAAAGCAATCAAGTGTGTTAAAGAGGCAAGCTTGAATGATGCAAGGTGCTCCT 490
Db 409 AAGGTGAAAAGCAATCAAGTGTGTTAAAGAGGCAAGCTTGAATGATGCAAGGTGCTCCT 468
QY 491 ATGTTGGAATTTGTTCTTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAA 550
Db 469 ATGTTGGAATTTGTTCTTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAA 528
QY 551 AAAAAA 560
Db 529 AAAAAA 538
RESULT 14
AAV18719
ID AAV18719 standard; cDNA; 541 BP.
XX
AC AAV18719;
XX
XX 30-JUL-1998 (first entry)
XX
DE cDNA encoding GAGE-4 tumour rejection antigen precursor.
XX
KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;
KW melanoma; antigen; cytolytic T cell clone proliferation;
KW HLA-typing assay; ss.
```

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XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX CDS 83..435
FT /*tag= a
FT /transl_except= (pos:197..199, aa:Ala)
FT /transl_except= (pos:200..202, aa:Thr)
XX
XX WO9749417-A1.
XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-US010850.
XX
XX 24-JUN-1996; 96US-00669161.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Debacker O, Van Den Eynde B, Boon-Falleur T;
XX
XX WPI; 1998-076905/07.
XX P-PSDB; AAW47601.
XX
XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -
XX processed by HLA-Cw6 molecules into peptides, useful to diagnose
XX melanomas.
XX
XX Example 13; Fig 4; 60pp; English.
XX
CC The present sequence encodes a GAGE-4 tumour tumour rejection antigen
CC precursor (TRAP). The protein is expressed in a number of tumours. In
CC contrast the only normal tissue which expresses GAGE TRAP protein is
CC testis. Several GAGE TRAPs have been identified (see AAV18717-21). The
CC major difference between these proteins and GAGE-1 (AAV05540) is the
CC absence of a stretch of 143 bases located at position 379 to 521 of the
CC GAGE-1 TRAP sequence. The rest of the sequences show mismatches at
CC various position, with the exception of GAGE-3 whose 5' end is totally
CC different from the other GAGE cDNAs for the first 112 bases. This region
CC of GAGE-3 cDNA contains a long repeat and a hairpin structure. The
CC antigens can be used to diagnose melanomas, characterised by expression
CC of a TRAP or presentation of a tumour rejection antigen. Antigens shed
CC into blood or urine can be observed and then used to confirm a diagnosis
CC of melanoma using cytolytic T cell clone proliferation methodologies.
CC Other uses for the processed peptides, include HLA-typing assays for,
CC e.g. skin graft or organ transplants
XX
SQ Sequence 541 BP; 158 A; 117 C; 154 G; 112 T; 0 U; 0 Other;
Query Match 76.0%; Score 425.8; DB 2; Length 541;
Best Local Similarity 98.2%; Pred. No. 2e-112;
Matches 441; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 113 GAGAAATCGACCTATTATGGCTAGACCAAGGCGCTATGTACAGCCTCTCAAGTGA 172
Db 93 GAGGAATCGACCTATTATTTGGCCTAGACCAAGGCGCTATGTACAGCCTCTCAAAATGA 152
QY 173 TTGGGCTATGCGGCCCGAGCAGTTTCAGTGTATGAAGTGAACCAACACCTCAAGAG 232
Db 153 TTGGGCTATGCGGCCCGAGCAGTTTCAGTGTATGAAGTGAACCAACAGCCTCTCAAGAG 212
QY 233 GGGAACCAAGCAACTCAACGTCAGGATCTCTGAGTGTCTCAGGAGGGAGGATGAGGAG 292
Db 213 GGGAACCAAGCAACTCAACGTCAGGATCTCTGAGTGTCTCAGGAGGGAGGATGAGGAG 272
QY 293 CATCTGAGGTCAAGGGCCGAGCCTGAAGCTGTATAGCAGGACAGGTCACCCACAGA 352
Db 273 CATCTGAGGTCAAGGGCCGAGCCTGAAGCTGTATAGCAGGACAGGTCACCCACAGA 332
QY 353 CTGGGTGTGAGTGTGAAGATGTTCTCTGATGGGAGGATGAGACCCGCAATTCAGAGG 412
Db 333 CTGGGTGTGAGTGTGAAGATGTTCTCTGATGGGAGGATGAGACCCGCAATTCAGAGG 392
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QY 413 AGCTGAAAACGGCTGAAGAGGTGAAAACATCACAGTGTGTTAAAGAGGACAGCTTG-A 471  
Db |||||  
QY 393 AGCTGAAAACGGCTGAAGAGGTGAAAACATCACAGTGTGTTAAAGAGGACAGCTTGAA 452  
Db |||||  
QY 472 AATGATGCGAGGCTGCTCCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAAAGCTT 531  
Db |||||  
QY 453 AATGATGCGAGGCTGCTCCTATGTTGGAATTTGTTTCAATAAATTTCTCCCAATAAAGCTT 512  
Db |||||  
QY 532 TACAGCCTTCTGCAAGGAAAAA 560  
Db |||||  
QY 513 TACAGCCTTCTGCAAGGAAAAA 541  
Db |||||  
RESULT 15  
ABZ20463  
ID ABZ20463 standard; cDNA; 530 BP.  
XX  
AC ABZ20463;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE GAGE-2 full length cDNA sequence SEQ ID NO:2890.  
XX  
KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
KW immune response; virology; immunology; microbiology; molecular biology;  
KW recombinant DNA technology; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200278516-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US010421.  
XX  
PR 30-MAR-2001; 2001US-0280255P.  
PR 28-AUG-2001; 2001US-0315563P.  
PR 09-JAN-2002; 2002US-0347313P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Wang T, Wang S, Bangur CS, Gaiger A;  
XX  
DR WPI; 2003-058387/05.  
DR P-PSDB; ABP54447.  
XX  
PT New immunogenic polynucleotides or polypeptides useful for diagnosing,  
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
PT virology, immunology, microbiology, molecular biology and recombinant DNA  
PT techniques.  
XX  
PS Claim 1; SEQ ID NO 2890; 207pp; English.  
XX  
CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
CC invention. (I) and (II) have cytostatic activity and can be used in gene  
CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques. N.B. The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 530 BP; 152 A; 116 C; 155 G; 107 T; 0 U; 0 Other;  
Query Match 75.2%; Score 421.2; DB 7; Length 530;  
Best Local Similarity 92.1%; Pred.No. 4.2e-111;  
Matches 444; Conservative 0; Mismatches 38; Indels 0; Gaps 0;  
QY 71 TCTTCTCGCCAACTCATATTTTCAACAGATGAATCTAGTAGAGGAAATCGACCTATT 130  
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Db 49 TCTTTTCTCTACTACTGAGATTCACTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCT 108  
QY 131 ATTGGCCTAGACCAAGGCGCTATGTACAGCCTCTCTGAAGTGAATTGGGCTTATCGGCCCCG 190  
Db 109 ATCGGCTTAGACCAAGACGCTAGTAGAGCTCTCTGAATGATTGGGCTTATCGGCCCCG 168  
QY 191 AGCAGTTTCAGTGTATGAGTGGAAACACGCAACACCTGAAAGAGGGGAAACGAGCAACTCAAC 250  
Db 169 AGCAGTTTCAGTGTATGAGTGGAAACACGCAACACCTGAAAGAGGGGAAACGAGCAACTCAAC 228  
QY 251 GTCAGGATCCTGCAGCTGCTCAGGAGGGAGAGGATGAGGAGGAGGATGAGGAGGATGAGGAGG 310  
Db 229 GTCAGGATCCTGCAGCTGCTCAGGAGGGAGAGGATGAGGAGGAGGATGAGGAGGATGAGGAGG 288  
QY 311 CGAAGCCTGAAGCTGATAGTCCAGGAAACAGGGTCAACCACAGACTTGGGTGTGAGTGTGAAG 370  
Db 289 CGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCAACCACAGACTTGGGTGTGAGTGTGAAG 348  
QY 371 ATGGTCTCTGATGGGAGGAGATGGACCCGCCAAAATCCAGAGGAGGAGGAGGAGGAGGAGGAG 430  
Db 349 ATGGTCTCTGATGGGAGGAGATGGACCCGCCAAAATCCAGAGGAGGAGGAGGAGGAGGAGGAG 408  
QY 431 AAGGTGAAAAGCAATCACAGTGTGTTAAAGAGGACAGGTTGAAATGATGACAGGCTGCTCCT 490  
Db 409 AAGGTGAAAAGCAATCACAGTGTGTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 468  
QY 491 ATGTTGGAAAATTTGTTTCATTAATAATTTCTCCCAATAAAGCTTTACAGCCTTTTCGAAAAGAA 550  
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QY 551 AA 552  
Db 529 AA 530

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
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# SUMMARIES

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2	540	100.0	540	6	BD231799	BD231799 Isolated
3	540	100.0	540	6	I55853	I55853 Sequence 16
4	540	100.0	540	6	BD132469	BD132469 Isolated
5	534.2	98.9	539	6	AR028492	AR028492 Sequence
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7	534.2	98.9	539	6	I55855	I55855 Sequence 18
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13	528.8	97.8	528	6	AX334151	AX334151 Sequence
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18	512.8	95.0	538	6	AR028488	AR028488 Sequence
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22	508.8	94.2	526	6	AR275666	AR275666 Sequence
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25	504.4	93.4	528	6	AR275665	AR275665 Sequence
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27	360.4	66.7	430	6	AX886264	AX886264 Sequence
28	360.4	66.7	430	6	BD25874	BD25874 Sequence
29	306.2	56.7	530	6	AX284300	AX284300 Sequence
30	304	56.3	365	6	AX284692	AX284692 Sequence
31	175.8	32.6	493	9	HSA318881	AJ318881 Homo sapi
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33	155.4	28.8	506	6	AR415772	AR415772 Sequence
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35	150.6	27.9	441	12	BT007722	BT007722 Synthetic
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# ALIGNMENTS

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LOCUS AR028490 Sequence 16 from patent US 5858689.  
DEFINITION AR028490  
ACCESSION AR028490  
VERSION AR028490.1 GI:5940463  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 540)  
AUTHORS van den Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Falleur,T.  
TITLE Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof

AR028490 540 bp DNA linear PAT 29-SEP-1999

JOURNAL Patent: US 5858689-A 16 12-JAN-1999;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 540; DB 6; Length 540;  
Best Local Similarity 100.0%; Pred. No. 2.8e-129; Indels 0; Gaps 0;  
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
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LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
DEFINITION as molecules encoding the same, and utilization thereof.  
ACCESSION BD231799.1 GI:33041569  
VERSION JP 2002509859-A/9  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 540)  
AUTHORS Bruggen, P.V.D., Bynde, B.V.D., DeBacker, O. and Falleur, T.B.  
TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof  
JOURNAL Patent: JP 2002509859-A 9 02-APR-2002;  
COMMENT LUDWIG INSTITUTE FOR CANCER RESEARCH  
OS Homo sapiens (human)  
PN JP 2002509859-A/9  
PD 02-APR-2002  
PF 02-APR-2002  
PR 23-JAN-1999 JP 2000528586  
PI PIERRE VAN DER BRUGEN, BENOIT VAN DEN EYNDE, OLIVIER DEBACKER, THIERRY BOON FALLEUR

PC C07K4/12, C12N15/09, C12P21/00, C12Q1/02, C12N15/00 CC  
Strandedness: Single;  
CC Topology: Linear;  
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PH Key Location/Qualifiers  
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/organism='Homo sapiens (human)'.  
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Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 TGGCAGGAGATGCAACCGCCAAATCCAGAGGAGTGAAGACGGCTCAAGAGGTTGAAAA 420  
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QY 421 GCAATCAAGTGTAAAGAGGACGTTGAAATGATGCGAGCTGCTCTATGTTGGAAA 480  
DB 421 GCAATCAAGTGTAAAGAGGACGTTGAAATGATGCGAGCTGCTCTATGTTGGAAA 480

QY 481 TTTGTTCAATTAATAATCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAA 540  
DB 481 TTTGTTCAATTAATAATCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAA 540

RESULT 3  
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LOCUS Sequence 16 from patent US 5648226.  
DEFINITION I55853  
ACCESSION I55853  
VERSION I55853.1 GI:2476647  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 540)  
AUTHORS Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.  
TITLE Isolated peptides derived from tumor rejection antigens, and their use  
JOURNAL Patent: US 5648226-A 16 15-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..540  
/organism="unknown"



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Best Local Similarity		100.0%; Pred. No. 2.8e-129;	
Matches 540; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	CGCCAGGAGCTGTGAGGAGTCTGTGTGTTCTCTGCGTCCGGACTCTTTTCTCTA	60
Db	1	CGCCAGGAGCTGTGAGGAGTCTGTGTGTTCTCTGCGTCCGGACTCTTTTCTCTA	60
QY	61	CTGAGATTTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATGACCTATTATTGGCTAG	120
Db	61	CTGAGATTTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATGACCTATTATTGGCTAG	120
QY	121	ACCAAGGCGCTATGTACAGCTCTCTGAAATGATTGGCGCTATGCGGCCGAGCAGTTTCA	180
Db	121	ACCAAGGCGCTATGTACAGCTCTCTGAAATGATTGGCGCTATGCGGCCGAGCAGTTTCA	180
QY	181	TGATGAAGTGGAAACCAAGCAACCTGAAGAGGGGAACCAAGCAACTCAACGTCAGGATCC	240
Db	181	TGATGAAGTGGAAACCAAGCAACCTGAAGAGGGGAACCAAGCAACTCAACGTCAGGATCC	240
QY	241	TGCAGCTGCTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGA	300
Db	241	TGCAGCTGCTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGA	300
QY	301	AGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGTGTGAGTGTGAAGATGGTCTGA	360
Db	301	AGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGTGTGAGTGTGAAGATGGTCTGA	360
QY	361	TGGCAGGAGATGGACCCGCCAAATCCAGAGAGGTGAAAACGCCCTGAAGAAGGTGAAA	420
Db	361	TGGCAGGAGATGGACCCGCCAAATCCAGAGAGGTGAAAACGCCCTGAAGAAGGTGAAA	420
QY	421	GCAATCACAGTGTAAAAGAGGCAAGTTGAAATGATGCAGGCTGCTCTATTGTTGAAA	480
Db	421	GCAATCACAGTGTAAAAGAGGCAAGTTGAAATGATGCAGGCTGCTCTATTGTTGAAA	480
QY	481	TTTGTTCATTAAATTCCTCCCAATAAGCTTTACAGCCTTCTGCAAAAAA	540
Db	481	TTTGTTCATTAAATTCCTCCCAATAAGCTTTACAGCCTTCTGCAAAAAA	540
RESULT 4			
BD132469		540 bp DNA linear PAT 18-SEP-2002	
LOCUS		Isolated, nucleic acid molecules which code for GAGE tumor	
DEFINITION		rejection antigen, the tumor rejection antigen, and uses thereof.	
ACCESSION		BD132469	
VERSION		JP 2002507112-A/9	
KEYWORDS		synthetic construct	
SOURCE		synthetic construct	
ORGANISM		artificial sequences.	
REFERENCE		1 (bases 1 to 540)	
AUTHORS		Debacker, O., Eynde, B.V.D. and Falleur, T.B.	
TITLE		Isolated, nucleic acid molecules which code for GAGE tumor	
JOURNAL		rejection antigen, the tumor rejection antigen, and uses thereof	
COMMENT		Patent: JP 2002507112-A 9 05-MAR-2002;	
FEATURES		LUDWIG INSTITUTE FOR CANCER RESEARCH	
source		FN JP 2002507112-A/9	
Location/Qualifiers		PD 05-MAR-2002	
Key		PR 23-JUN-1997 JP 1998503430	
Key		PF 24-JUN-1996 US 08/669161	
Key		PI OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON, FALLEUR PC	
Key		A61K38/00, A61K45/05, C07K7/00, C07K14/82, C12N15/00 CC	
Key		Strandedness: Single;	
Key		CC Topology: Linear;	
Key		FH Key Location/Qualifiers.	
Key		1. .540	
Key		/organism="synthetic construct"	
Query Match		98.9%; Score 534.2; DB 6; Length 539;	
Best Local Similarity		99.4%; Pred. No. 8.9e-128;	
Matches 536; Conservative		0; Mismatches 3; Indels 0; Gaps 0;	
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ORIGIN		/mol_type="genomic DNA"	
Query Match		100.0%; Score 540; DB 6; Length 540;	
Best Local Similarity		100.0%; Pred. No. 2.8e-129;	
Matches 540; Conservative			0; Mismatches 0; Indels 0; Gaps 0;
QY	1	CGCCAGGAGCTGTGAGGAGTCTGTGTGTTCTCTGCGTCCGGACTCTTTTCTCTA	60
Db	1	CGCCAGGAGCTGTGAGGAGTCTGTGTGTTCTCTGCGTCCGGACTCTTTTCTCTA	60
QY	61	CTGAGATTTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATGACCTATTATTGGCTAG	120
Db	61	CTGAGATTTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATGACCTATTATTGGCTAG	120
QY	121	ACCAAGGCGCTATGTACAGCTCTCTGAAATGATTGGCGCTATGCGGCCGAGCAGTTTCA	180
Db	121	ACCAAGGCGCTATGTACAGCTCTCTGAAATGATTGGCGCTATGCGGCCGAGCAGTTTCA	180
QY	181	TGATGAAGTGGAAACCAAGCAACCTGAAGAGGGGAACCAAGCAACTCAACGTCAGGATCC	240
Db	181	TGATGAAGTGGAAACCAAGCAACCTGAAGAGGGGAACCAAGCAACTCAACGTCAGGATCC	240
QY	241	TGCAGCTGCTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGA	300
Db	241	TGCAGCTGCTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGA	300
QY	301	AGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGTGTGAGTGTGAAGATGGTCTGA	360
Db	301	AGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGTGTGAGTGTGAAGATGGTCTGA	360
QY	361	TGGCAGGAGATGGACCCGCCAAATCCAGAGAGGTGAAAACGCCCTGAAGAAGGTGAAA	420
Db	361	TGGCAGGAGATGGACCCGCCAAATCCAGAGAGGTGAAAACGCCCTGAAGAAGGTGAAA	420
QY	421	GCAATCACAGTGTAAAAGAGGCAAGTTGAAATGATGCAGGCTGCTCTATTGTTGAAA	480
Db	421	GCAATCACAGTGTAAAAGAGGCAAGTTGAAATGATGCAGGCTGCTCTATTGTTGAAA	480
QY	481	TTTGTTCATTAAATTCCTCCCAATAAGCTTTACAGCCTTCTGCAAAAAA	540
Db	481	TTTGTTCATTAAATTCCTCCCAATAAGCTTTACAGCCTTCTGCAAAAAA	540
RESULT 5			
AR028492		539 bp DNA linear PAT 29-SEP-1999	
LOCUS		Sequence 18 from patent US 5858689.	
DEFINITION		AR028492	
ACCESSION		AR028492.1 GI:5940465	
VERSION		Unknown.	
KEYWORDS		Unknown.	
SOURCE		Unclassified.	
ORGANISM		1 (bases 1 to 539)	
REFERENCE		van der Bruggen, P., van den Eynde, B., DeBacker, O. and	
AUTHORS		Boon-Falleur, T.	
TITLE		Isolated peptides derived from the gage tumor rejection antigen	
JOURNAL		precursor and uses thereof	
FEATURES		Patent: US 5858689-A 18 12-JAN-1999;	
source		Location/Qualifiers	
Location/Qualifiers		1. .539	
Key		/organism="unknown"	
Key		/mol_type="unassigned DNA"	

Db 1 GCCAGGAGCTGTGAGCAGTCTGTGTGTTCTTCCGCGTCCGACTCTTTTCTCTAC 60  
QY 62 TGAGATTCACTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTTAC 121  
Db 61 TGAGATTCACTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTTAC 120  
QY 122 CCAAGCGGTATGTACAGCTCTGAAATGATTGGGCTTATGCGGCCGAGCAGTTTCACT 181  
Db 121 CCAAGCGGTATGTACAGCTCTGAAATGATTGGGCTTATGCGGCCGAGCAGTTTCACT 180  
QY 182 GATGAAGTGAACACAGCAACCTGAAAGAGGGAACACAGCAACTCAACGTACAGATCCT 241  
Db 181 GATGAAGTGAACACAGCAACCTGAAAGAGGGAACACAGCAACTCAACGTACAGATCCT 240  
QY 242 GAGCTGCTCAGAGGAGGAGTATGAGGAGCATCTGCAGTCAAGGCCGAGCCTGAA 301  
Db 241 GAGCTGCTCAGAGGAGGAGTATGAGGAGCATCTGCAGTCAAGGCCGAGCCTGAA 300  
QY 302 GCTGATAGCCAGGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 361  
Db 301 GCTGATAGCCAGGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 360  
QY 362 GGGCAGGAGTGAACCCGCAATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAAG 421  
Db 361 GGGCAGGAGTGAACCCGCAATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAAG 420  
QY 422 CAATCAGTGTAAAGAGGACGTTGAAATGATGAGGCTCTCTATGTTGAAAT 481  
Db 421 CAATCAGTGTAAAGAGGACGTTGAAATGATGAGGCTCTCTATGTTGAAAT 480  
QY 482 TTGTTCAATTAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 540  
Db 481 TTGTTCAATTAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 539

RESULT 6  
BD231801 539 bp DNA linear PAT 17-JUL-2003  
LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
DEFINITION as molecules encoding the same, and utilization thereof.  
ACCESSION BD231801.1 GI:33041571  
VERSION JP 2002509859-A/11.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
AUTHORS Bruggen,P.V.D., Eynde,B.V.D., Debacker,O. and Falleur,T.B.  
TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
as molecules encoding the same, and utilization thereof  
JOURNAL Patent: JP 2002509859-A 11 02-APR-2002;  
LUDWIG INSTITUTE FOR CANCER RESEARCH  
COMMENT OS Homo sapiens (human)  
PN JP 2002509859-A/11  
PD 02-APR-2002  
PF 12-JAN-1999 JP 2000528586  
PI 23-JAN-1998 US 09/012818  
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,  
PI THIERRY BOON FALLEUR  
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC  
Strandedness: Single;  
CC Topology: linear;  
CC STRANDEDNESS:single,TOPOLOGY:linear  
FH Key Location/Qualifiers  
FT source 1..539  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source 1..539  
/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'  
ORIGIN

Query Match 98.9%; Score 534.2; DB 6; Length 539;  
Best Local Similarity 99.4%; Pred. No. 8.9e-128;  
Matches 536; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GCCAGGAGCTGTGAGCAGTCTGTGTGTTCTTCCGCGTCCGACTCTTTTCTCTAC 61  
Db 1 GCCAGGAGCTGTGAGCAGTCTGTGTGTTCTTCCGCGTCCGACTCTTTTCTCTAC 60  
QY 62 TGAGATTCACTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTTAC 121  
Db 61 TGAGATTCACTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTTAC 120  
QY 122 CCAAGCGGTATGTACAGCTCTGAAATGATTGGGCTTATGCGGCCGAGCAGTTTCACT 181  
Db 121 CCAAGCGGTATGTACAGCTCTGAAATGATTGGGCTTATGCGGCCGAGCAGTTTCACT 180  
QY 182 GATGAAGTGAACACAGCAACCTGAAAGAGGGAACACAGCAACTCAACGTACAGATCCT 241  
Db 181 GATGAAGTGAACACAGCAACCTGAAAGAGGGAACACAGCAACTCAACGTACAGATCCT 240  
QY 242 GAGCTGCTCAGAGGAGGAGTATGAGGAGCATCTGCAGTCAAGGCCGAGCCTGAA 301  
Db 241 GAGCTGCTCAGAGGAGGAGTATGAGGAGCATCTGCAGTCAAGGCCGAGCCTGAA 300  
QY 302 GCTGATAGCCAGGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 361  
Db 301 GCTGATAGCCAGGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 360  
QY 362 GGGCAGGAGTGAACCCGCAATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAAG 421  
Db 361 GGGCAGGAGTGAACCCGCAATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAAG 420  
QY 422 CAATCAGTGTAAAGAGGACGTTGAAATGATGAGGCTCTCTATGTTGAAAT 481  
Db 421 CAATCAGTGTAAAGAGGACGTTGAAATGATGAGGCTCTCTATGTTGAAAT 480  
QY 482 TTGTTCAATTAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 540  
Db 481 TTGTTCAATTAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 539  
RESULT 7  
I55855 539 bp DNA linear PAT 07-OCT-1997  
LOCUS Sequence 18 from patent US 5648226.  
DEFINITION I55855  
ACCESSION I55855  
VERSION I55855.1 GI:2476649  
KEYWORDS Unknown.  
SOURCE Unclassified.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 539)  
AUTHORS Van den Eynde B., DeBacker O. and Boon-Falleur, T.  
TITLE Isolated peptides derived from tumor rejection antigens, and their use  
JOURNAL Patent: US 5648226-A 18 15-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..539  
/organism='unknown'  
/mol\_type='unassigned DNA'  
ORIGIN  
Query Match 98.9%; Score 534.2; DB 6; Length 539;  
Best Local Similarity 99.4%; Pred. No. 8.9e-128;  
Matches 536; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GCCAGGAGCTGTGAGCAGTCTGTGTGTTCTTCCGCGTCCGACTCTTTTCTCTAC 61  
Db 1 GCCAGGAGCTGTGAGCAGTCTGTGTGTTCTTCCGCGTCCGACTCTTTTCTCTAC 60  
QY 62 TGAGATTCACTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTTAC 121



QY 249 CTCAGAGGAGGAGGATGAGGAGCATCTCGAGTCAAGGCGCGAAGCCCTGAAGCTGATA 308  
 Db 241 CTCAGAGGAGGAGGATGAGGAGCATCTCGAGTCAAGGCGCGAAGCCCTGAAGCTGATA 300  
 QY 309 GCCAGGAAACAGGGTCAACCAACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGCAGG 368  
 Db 301 GCCAGGAAACAGGGTCAACCAACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGCAGG 360  
 QY 369 AGATGACCGCGCCAAATCCAGAGGAGGTGAAACCGCTGAAGAGTGAAGCAATCAC 428  
 Db 361 AGATGACCGCGCCAAATCCAGAGGAGGTGAAACCGCTGAAGAGTGAAGCAATCAC 420  
 QY 429 AGTGTAAAAGAGGACGCTTGAATCATGACAGCTGCTCTCTATGTTGGAAATTTGTTCA 488  
 Db 421 AGTGTAAAAGAGGACGCTTGAATCATGACAGCTGCTCTCTATGTTGGAAATTTGTTCA 480  
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 Db 481 TTAATAATTCCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAAAGAAAAA 532

RESULT 10  
 BD231800 532 bp DNA linear PAT 17-JUL-2003  
 LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
 DEFINITION as molecules encoding the same, and utilization thereof.

ACCESSION BD231800.1 GI:33041570  
 VERSION JP 2002509859-A/10.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Bruggen,P.V.D., Eynde,B.V.D., DeBacker,O. and Faillier,T.B.  
 Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
 as molecules encoding the same, and utilization thereof  
 Patent: JP 2002509859-A 10 02-APR-2002;  
 JOURNAL LUDWIG INSTITUTE FOR CANCER RESEARCH  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002509859-A/10  
 PD 02-APR-2002  
 PF 12-JAN-1999 JP 2000528586  
 PR 23-JAN-1998 US 09/012818  
 PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,  
 PC THIERRY BOON FALLEUR  
 PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC  
 Strandedness: Single;  
 CC Topology: Linear;  
 CC STRANDEDNESS:single,TOPOLOGY:linear  
 FH Key Location/Qualifiers  
 FT source 1..532  
 FT /organism='Homo sapiens (human)'.  
 FT Location/Qualifiers  
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 /mol\_type='genomic DNA'  
 /db\_xref='taxon:9606'

ORIGIN  
 Query Match 97.9%; Score 528.8; DB 6; Length 532;  
 Best Local Similarity 99.6%; Pred. No. 2.2e-126;  
 Matches 530; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 AGCTGTGAGGAGTGTGTGGTCTCTGCGTCCGACTCTTTTCTCTACTGAGATT 68  
 Db 1 AGCTGTGAGGAGTGTGTGGTCTCTGCGTCCGACTCTTTTCTCTACTGAGATT 60  
 QY 69 CATCTGTGAAATATGATGTTGGCAGGAGATCGACCTATTATTGGCCTAGACCAAGGC 128  
 Db 61 CATCTGTGAAATATGATGTTGGCAGGAGATCGACCTATTATTGGCCTAGACCAAGGC 120

QY 129 GCTATGTACAGCCTCTCTGAAATGATTGGCCCTATGCGGCCCGAGCAGTTCAGTGTGTAAG 188  
 Db 121 GCTATGTACAGCCTCTCTGAAATGATTGGCCCTATGCGGCCCGAGCAGTTCAGTGTGTAAG 180  
 QY 189 TGGAAACCAACACCTGTAAGAGGGGAACCAAGCAACTCAACGTCAAGATCTCTGACGCTG 248  
 Db 181 TGGAAACCAACACCTGTAAGAGGGGAACCAAGCAACTCAACGTCAAGATCTCTGACGCTG 240  
 QY 249 CTCAGGAGGAGGAGGATGAGGAGCATCTCGAGTCAAGGCGCGAAGCCCTGAAGCTGATA 308  
 Db 241 CTCAGGAGGAGGAGGATGAGGAGCATCTCGAGTCAAGGCGCGAAGCCCTGAAGCTGATA 300  
 QY 309 GCCAGGAAACAGGGTCAACCAACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGCAGG 368  
 Db 301 GCCAGGAAACAGGGTCAACCAACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGCAGG 360  
 QY 369 AGATGACCGCGCCAAATCCAGAGGAGGTGAAACCGCTGAAGAGTGAAGCAATCAC 428  
 Db 361 AGATGACCGCGCCAAATCCAGAGGAGGTGAAACCGCTGAAGAGTGAAGCAATCAC 420  
 QY 429 AGTGTAAAAGAGGACGCTTGAATCATGACAGCTGCTCTCTATGTTGGAAATTTGTTCA 488  
 Db 421 AGTGTAAAAGAGGACGCTTGAATCATGACAGCTGCTCTCTATGTTGGAAATTTGTTCA 480  
 QY 489 TTAATAATTCCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAAAGAAAAA 540  
 Db 481 TTAATAATTCCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAAAGAAAAA 532

RESULT 11  
 I55854  
 LOCUS Sequence 17 from patent US 5648226.  
 DEFINITION 532 bp DNA linear PAT 07-OCT-1997  
 ACCESSION I55854  
 VERSION I55854.1 GI:2476648  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 532)  
 AUTHORS Van den Bynde,B., DeBacker,O. and Boon-Falleur,T.  
 TITLE Isolated peptides derived from tumor rejection antigens, and their use  
 JOURNAL Patent: US 5648226-A 17 15-JUL-1997;  
 FEATURES Location/Qualifiers  
 source 1..532  
 /organism='unknown'  
 /mol\_type='unassigned DNA'

ORIGIN  
 Query Match 97.9%; Score 528.8; DB 6; Length 532;  
 Best Local Similarity 99.6%; Pred. No. 2.2e-126;  
 Matches 530; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 AGCTGTGAGGAGTGTGTGGTCTCTGCGTCCGACTCTTTTCTCTACTGAGATT 68  
 Db 1 AGCTGTGAGGAGTGTGTGGTCTCTGCGTCCGACTCTTTTCTCTACTGAGATT 60  
 QY 69 CATCTGTGAAATATGATGTTGGCAGGAGATCGACCTATTATTGGCCTAGACCAAGGC 128  
 Db 61 CATCTGTGAAATATGATGTTGGCAGGAGATCGACCTATTATTGGCCTAGACCAAGGC 120  
 QY 129 GCTATGTACAGCCTCTCTGAAATGATTGGCCCTATGCGGCCCGAGCAGTTCAGTGTGTAAG 188  
 Db 121 GCTATGTACAGCCTCTCTGAAATGATTGGCCCTATGCGGCCCGAGCAGTTCAGTGTGTAAG 180  
 QY 189 TGGAAACCAACACCTGTAAGAGGGGAACCAAGCAACTCAACGTCAAGATCTCTGACGCTG 248  
 Db 181 TGGAAACCAACACCTGTAAGAGGGGAACCAAGCAACTCAACGTCAAGATCTCTGACGCTG 240  
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 Db 241 CTCAGGAGGAGGAGGATGAGGAGCATCTCGAGTCAAGGCGCGAAGCCCTGAAGCTGATA 300

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QY 309 GCAGGAAACAGGTCACCCACAGACTGGGTGCTGAGTGTGAAGATGTCCTGATGGGAGG 368
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Db 361 AGATGACCCGCCAAATCCAGAGGAGGTGAAAACGCTGAGAAGGTGAAAAGCAATCAC 420
QY 429 AGTGTATAAAGAGGACGTTGAAATGATGACGGCTGCTCTATGTTGGAATTTGTTCA 488
Db 421 AGTGTATAAAGAGGACGTTGAAATGATGACGGCTGCTCTATGTTGGAATTTGTTCA 480
QY 489 TTAATAATTCCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAAATAAAAAA 540
Db 481 TTAATAATTCCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAAATAAAAAA 532

RESULT 12
BD132470 532 bp DNA linear PAT 18-SEP-2002
LOCUS Isolated, nucleic acid molecules which code for GAGE tumor
DEFINITION rejection antigen, the tumor rejection antigen, and uses thereof.
ACCESSION BD132470
VERSION JP 2002507112-A/10.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 532)
AUTHORS Debacter,O., Bynde,B.V.D. and Falleur,T.B.
TITLE Isolated, nucleic acid molecules which code for GAGE tumor
JOURNAL rejection antigen, the tumor rejection antigen, and uses thereof
PATENT: JP 2002507112-A 10 05-MAR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT PN JP 2002507112-A/10
PD 05-MAR-2002
PF 23-JUN-1997 JP 1998503430
PR 24-JUN-1996 US 08/669161
PI OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIERRY BOON FALLEUR PC
A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source
1..532
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 97.9%; Score 528.8; DB 6; Length 532;
Best Local Similarity 99.6%; Pred. No. 2.2e-126;
Matches 530; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 AGCTGTAGGCGAGTCTGTGTGCTTCCTGCCCTCCGACTCTTTTCTCTACTCAGATT 68
Db 1 AGCTGTAGGCGAGTCTGTGTGCTTCCTGCCCTCCGACTCTTTTCTCTACTCAGATT 60
QY 69 CATCTGTGTAATATGATTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 128
Db 61 CATCTGTGTAATATGATTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 120
QY 129 GCTATGTACAGCTCCTGAAATGATTGGCCCTATCGGCCCGAGCAGTTCACTGATGAAG 188
Db 121 GCTATGTACAGCTCCTGAAATGATTGGCCCTATCGGCCCGAGCAGTTCACTGATGAAG 180
QY 189 TGGAAACCAAGCAACCTGAAGAAGGGGAACCAAGCAACTCAAGTCAGAGTCTCGAGCTG 248
Db 181 TGGAAACCAAGCAACCTGAAGAAGGGGAACCAAGCAACTCAAGTCAGAGTCTCGAGCTG 240
QY 249 CTCAGAGGAGGATGAGGAGGATCTGTCAGGTCAAGGGCCGAAGCCTGAAGCTGATA 308

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Db 241 CTCAGGAGGAGAGGATGAGGGAGCACTCTGCAAGTCAAGGCCCAAGACCTGAAGCTGATA 300
QY 309 GCAGGAAACAGGTCACCCACAGACTGGGTGCTGAGTGTGAAGATGTCCTGATGGGAGG 368
Db 301 GCCAGAAACAGGTCACCCACAGACTGGGTGCTGAGTGTGAAGATGTCCTGATGGGAGG 360
QY 369 AGATGACCCGCCAAATCCAGAGGAGGTGAAAACGCTGAGAAGGTGAAAAGCAATCAC 428
Db 361 AGATGACCCGCCAAATCCAGAGGAGGTGAAAACGCTGAGAAGGTGAAAAGCAATCAC 420
QY 429 AGTGTATAAAGAGGACGTTGAAATGATGACGGCTGCTCTATGTTGGAATTTGTTCA 488
Db 421 AGTGTATAAAGAGGACGTTGAAATGATGACGGCTGCTCTATGTTGGAATTTGTTCA 480
QY 489 TTAATAATTCCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAAATAAAAAA 540
Db 481 TTAATAATTCCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAAATAAAAAA 532

RESULT 13
AX334151 528 bp DNA linear PAT 09-JAN-2002
LOCUS Sequence 4660 from Patent WO0194629.
DEFINITION AX334151
ACCESSION AX334151
VERSION AX334151.1 GI:18124870
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL gene sets
PATENT: WO 0194629-A 4660 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source
1..528
/organism="Homo sapiens"
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ORIGIN
Query Match 97.8%; Score 528; DB 6; Length 528;
Best Local Similarity 100.0%; Pred. No. 3.6e-126;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCAGGAGCTGTGAGGAGTCTGTGTGTTCTGCGCTCCGACTCTTTTCTCTCTA 60
Db 1 CGCCAGGAGCTGTGAGGAGTCTGTGTGTTCTGCGCTCCGACTCTTTTCTCTCTA 60
QY 61 CTGAGATTCACTGTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG 120
Db 61 CTGAGATTCACTGTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG 120
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Db 121 ACCAAGCGCTATGTACAGCCTCTGAAATGATTGGGCTATGGCGCCGAGCAGTTTCAG 180
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Db      361 TGGGAGGAGATGACCCGCAATTCAGAGGAGGTGAAACCCCTGAAGAGGTGAAA 420
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RESULT 14
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LOCUS      Human GAGE-4 protein mRNA, complete cds.
DEFINITION      U19145
ACCESSION      U19145
VERSION      U19145.1 GI:914904
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 528)
AUTHORS      Van den Eynde,B., Peeters,O., De Backer,O., Gauglier,B., Lucas,S.
and Boon,T.
TITLE      A new family of genes coding for an antigen recognized by
autologous cytolytic T lymphocytes on a human melanoma
J. Exp. Med. 182 (3), 689-698 (1995)
JOURNAL
MEDLINE      95378788
PUBMED      7544395
REFERENCE      2 (bases 1 to 528)
AUTHORS      Van den Eynde,B.J.
Direct Submission
TITLE      Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
JOURNAL
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Best Local Similarity 100.0%; Pred. No. 3.6e-126;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS      Human GAGE-6 protein mRNA, complete cds.
DEFINITION      U19147
ACCESSION      U19147.1 GI:914908
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 527)
AUTHORS      Van den Eynde,B., Peeters,O., De Backer,O., Gauglier,B., Lucas,S.
and Boon,T.
TITLE      A new family of genes coding for an antigen recognized by
autologous cytolytic T lymphocytes on a human melanoma
J. Exp. Med. 182 (3), 689-698 (1995)
JOURNAL
MEDLINE      95378788
PUBMED      7544395
REFERENCE      2 (bases 1 to 527)
AUTHORS      Van den Eynde,B.J.
Direct Submission
TITLE      Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
JOURNAL
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Matches 524; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db |||
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Db |||
QY 181 GATGAAGTGAACCCAGCAACACCTGAGAGAGGGGAAACCAGCAACTCAAAGTCAGGATCCT 240
QY 242 GCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGAGGTCAAGGCCGAGACCTGAA 301
Db |||
QY 241 GCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGAGGTCAAGGGCCGAGACCTGAA 300
QY 302 GCTGATAGCCAGGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGAT 361
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QY 362 GGGCAGGAGATGGACCCGCCAATCCAGAGGAGGTGAAAACGCTGAAAGGTGAAAAG 421
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Job time : 2251 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 13:18:49 ; Search time 2416 Seconds

(without alignments)  
6674.494 Million cell updates/sec

Title: US-09-782-745-16

Perfect score: 540

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 28726800

Minimum DB seq length: 0

Maximum DB seq length: 540

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em estba:\*

2: em esthum:\*

3: em estin:\*

4: em estmu:\*

5: em estov:\*

6: em estpl:\*

7: em estro:\*

8: em htc:\*

9: gb est1:\*

10: gb est2:\*

11: gb htc:\*

12: gb est3:\*

13: gb est4:\*

14: gb est5:\*

15: em estfun:\*

16: em estom:\*

17: em gss\_hum:\*

18: em gss\_inv:\*

19: em gss\_pln:\*

20: em gss\_vrt:\*

21: em gss\_fun:\*

22: em gss\_nam:\*

23: em gss\_mus:\*

24: em gss\_pro:\*

25: em gss\_rod:\*

26: em gss\_phg:\*

27: em gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	530.6	98.3	537	12	BM832793
2	514.2	95.2	527	12	BI826605
3	513.6	95.1	521	13	BI108227
4	508.2	94.1	517	14	CF780547

5	498.2	92.3	509	12	BI868671
6	473.2	87.6	489	9	AA447559
7	455.4	84.3	457	10	AW510753
8	446.8	82.7	464	9	AA738037
9	442.2	81.9	447	9	AI381509
10	438.6	81.2	480	12	BGI20336
11	437.6	81.0	505	14	CB115693
12	431.6	79.9	450	9	AA760996
13	420.2	77.8	455	9	AI187350
14	410.6	76.0	418	9	AW016546
15	402	74.4	426	9	AA868226
16	379.4	70.3	383	12	BM836228
17	379.2	70.2	419	9	AA448542
18	378.6	70.1	445	11	BC005363
19	363.8	67.4	412	9	AW102587
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22	318.8	59.0	397	12	BG206349
23	317.4	58.8	341	12	BP431265
24	315.6	58.4	398	9	AA918604
25	310.4	57.5	320	12	BM836021
26	308.8	57.2	333	13	BUS33718
27	276.2	51.1	457	14	CF780497
28	271.4	50.3	275	14	CB147043
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31	248.8	46.1	256	12	BG181480
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33	225	41.7	253	12	BG184057
34	225	41.7	261	12	BG190600
35	221.6	41.0	245	12	BG212621
36	218.2	40.4	292	12	BG212622
37	214.8	39.8	245	12	BG208433
38	209.2	38.7	507	9	AA972716
39	208	38.5	224	9	AA738394
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45	192.4	35.6	499	12	BG354572

## ALIGNMENTS

RESULT 1	BM832793	537 bp	mRNA	linear	EST 06-MAR-2002
BM832793	K-EST0107334	S5SNU484s1	Homo sapiens	CDNA clone	S5SNU484s1-8-F10
LOCUS	5', mRNA sequence.				
DEFINITION	BM832793				
ACCESSION	BM832793				
VERSION	BM832793.1				
KEYWORDS	EST				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.				
TITLE	21C Frontier Korean EST Project 2001				
JOURNAL	Unpublished (2002)				
COMMENT	Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 8 row: F column: 10 High quality sequence stop: 537.				

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CB115693 K-EST0159  
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AI187350 gf29a05.x  
AW016546 UI-H-BIOP  
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BM836228 K-EST0111  
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/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was decapped with tobacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dR)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10P with electroporation method."

## ORIGIN

Query Match 98.3%; Score 530.6; DB 12; Length 537;  
Best Local Similarity 99.3%; Pred. No. 1.5e-98;  
Matches 533; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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421 CAATCACAGTGTAAAGAGGACGTTGAAATGATGAGGCTGCTCTCTATTTGGAAAT 480  
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## RESULT 2

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LOCUS 60307056F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:516892 5',  
DEFINITION mRNA sequence.

ACCESSION BI826605  
VERSION BI826605.1 GI:15938155  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 527)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11419 row: p column: 13  
High quality sequence stop: 519.

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## ORIGIN

Query Match 95.2%; Score 514.2; DB 12; Length 527;  
Best Local Similarity 98.5%; Pred. No. 3.3e-95;  
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RESULT 3  
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 ACCESSION BX108227  
 VERSION BX108227.1 GI:27835080  
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 ORGANISM Homo sapiens  
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 1 (bases 1 to 521)  
 Eberl, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
 Radelof, U., Schneider, D. and Korn, B.  
 Human Unigeneset - RZPD3  
 Unpublished (2003)  
 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
 RZPD; IMAGE998K213161.  
 http://www.rzpd.de/Clonecards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de

This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, Primer sequence: TTTCACAGAAACAGCTATGAC.

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 /clone="IMAGE998K213161 ; IMAGE:1256204"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP GC3"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; 1st strand cDNA was prepared from 3 pooled  
 germ cell tumors, and was then primed with a Not I -  
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pT7T3  
 vector. Library is not normalized. Library was  
 constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 95.1%; Score 513.6; DB 13; Length 521;  
 Best Local Similarity 99.2%; Pred. No. 4.4e-95;  
 Matches 516; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 19 CAGTGTGTGTGTTCTCCGCTCCGACTCTTTTTCCTCTAGATTCATCTGTGTG 78  
 Db 1 CAGTGTGTGTGTTCTCCGCTCCGACTCTTTTTCCTCTAGATTCATCTGTGTG 60  
 QY 79 AAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGCGCTGTATACA 138  
 Db 61 AAATATGAGTTGGCGAGGAAGATCGACCTGTATTGGCCTAGTCCAAAGAGCTATCTACA 120  
 QY 139 GCCTCTGAAATGATTTGGCCTATGGGCCCGAGCAGTTTCAGTGTAAATGGAAACGAGC 198  
 Db 121 GCCTCTGAAATGATTTGGCCTATGCAGCCCGAGCAGTTTCAGTGTAAATGGAAACGAGC 180  
 QY 199 AACACCTGAAGAAGGGGAACCAAGCACTCAAGCTCAGGATCTCGCAGCTGCTCAGGAGG 258  
 Db 181 AACACCTGAAGAAGGGGAACCAAGCACTCAAGCTCAGGATCTCGCAGCTGCTCAGGAGG 240  
 QY 259 AGAGGATGAGGAGCATCTGCAGTCAAGGCCCGAGCCTGAAGCTGTATAGCCAGGAACA 318  
 Db 241 AGAGGATGAGGAGCATCTGCAGTCAAGGCCCGAGCCTGAAGCTGTATAGCCAGGAACA 300  
 QY 319 GGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGCAGAGATGGACCC 378  
 Db 301 GGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGCAGAGATGGACCC 360  
 QY 379 GCCAAATCCAGAGGAGTGAACCCCTGAAGAGTGAAGCAATCACAGTGTAAAAA 438  
 Db 361 GCCAAATCCAGAGGAGTGAACCCCTGAAGAGTGAAGCAATCACAGTGTAAAAA 420  
 QY 439 GAAGCAGCTTGAAATGATGCAGGCTGCTCTATGTGGAAATTTGTCATTAAATTTCT 498  
 Db 421 GAAGCAGCTTGAAATGATGCAGGCTGCTCTATGTGGAAATTTGTCATTAAATTTCT 480  
 QY 499 CCCAATAAGCTTTACAGCCTTCTGCAAAAAA 538  
 Db 481 CCCAATAAGCTTTACAGCCTTCTGCAAAAAA 520

CF780547 517 bp mRNA linear EST 20-OCT-2003  
 AGENCOURT 15739102 NIH MGC.217 Homo sapiens cDNA clone  
 IMAGE:30524555 5', mRNA sequence.

CF780547

CF780547.1 GI:37739989

EST.

Source Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 517)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: James Martin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM604 row: e column: 12

High quality sequence stop: 517.

Location/Qualifiers

## FEATURES



```

Db      487  TTTGTCATTAATAATCTCCAA 509
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AA447559      489 bp      mRNA      linear      EST 04-JUN-1997
zw81ell.sl Soares testis NHT Homo sapiens cDNA clone IMAGE:782636
3', similar to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ;, mRNA
sequence.
AA447559.1 GI:2161229
EST.
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 427.
Location/Qualifiers
1..489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:782636"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5]
TGTTACCAATCTGAAGTGGAGCGCGGCCCAATTTTTTTTTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaudo."

ORIGIN
Query Match      87.6%; Score 473.2; DB 9; Length 489;
Best Local Similarity 99.2%; Pred. No. 8.4e-87;
Matches 486; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 42  CCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTGAATATGATTGGCAGGAAGAT 101
|||||
Db 489  CCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTGAATATGATTGGCAGGAAGAT 430
|||||
QY 102  CGACCTATTATTGGCTAGACCAAGCGCTATGTATACAGCTCTCTGAAATGATTGGCCCTA 161
|||||
Db 429  CGACCTATTATTGGCCCTAGACCAAGCGCTATGTATACAGCTCTCTGAAATGATT-GGCCTA 371
|||||
QY 162  TCGGGCCCGCAGCTTCAGTGTAGTGTGAACACAGCAACCTGAGGAAGGGGACCGAG 221
|||||
Db 370  TCGGGCCCGCAGCTTCAGTGTAGTGTGAACACAGCAACCTGAGGAAGGGGACCGAG 311
|||||
QY 222  CAACTCAACGTTCAGGATCTCGAGCTGCTCAGGAGGAGGATGAGGGAGCATCTGCAG 281
|||||

RESULT 6
AA447559/c
LOCUS
DEFINITION
ACCESSION
AA447559.1 GI:2161229
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 427.
Location/Qualifiers
1..489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:782636"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5]
TGTTACCAATCTGAAGTGGAGCGCGGCCCAATTTTTTTTTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaudo."

ORIGIN
Query Match      87.6%; Score 473.2; DB 9; Length 489;
Best Local Similarity 99.2%; Pred. No. 8.4e-87;
Matches 486; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 42  CCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTGAATATGATTGGCAGGAAGAT 101
|||||
Db 489  CCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTGAATATGATTGGCAGGAAGAT 430
|||||
QY 102  CGACCTATTATTGGCTAGACCAAGCGCTATGTATACAGCTCTCTGAAATGATTGGCCCTA 161
|||||
Db 429  CGACCTATTATTGGCCCTAGACCAAGCGCTATGTATACAGCTCTCTGAAATGATT-GGCCTA 371
|||||
QY 162  TCGGGCCCGCAGCTTCAGTGTAGTGTGAACACAGCAACCTGAGGAAGGGGACCGAG 221
|||||
Db 370  TCGGGCCCGCAGCTTCAGTGTAGTGTGAACACAGCAACCTGAGGAAGGGGACCGAG 311
|||||
QY 222  CAACTCAACGTTCAGGATCTCGAGCTGCTCAGGAGGAGGATGAGGGAGCATCTGCAG 281
|||||

RESULT 7
AA510753/c
LOCUS
DEFINITION
ACCESSION
AA510753.1 GI:7148831
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 457)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..457
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2911881"
/lab_host="DH10B"
/clone_lib="Soares NFL T_GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaudo."

ORIGIN
Query Match      84.3%; Score 455.4; DB 10; Length 457;
Best Local Similarity 99.8%; Pred. No. 3.7e-83;
Matches 456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 76 GTCAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGT 135  
 Db 457 GTGAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGT 398  
 QY 136 ACAGCCTCTGAATGATTTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAGTGGAAAC 195  
 Db 397 ACAGCCTCTCTGAATGATTTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAGTGGAAAC 338  
 QY 196 AGCAACACCTTGAAGAGGGGAAACAGCAACTCAACGTCAGAGTCCCTGCAGCTCTCAGGA 255  
 Db 337 AGCAACACCTTGAAGAGGGGAAACAGCAACTCAACGTCAGAGTCCCTGCAGCTCTCAGGA 278  
 QY 256 GCGAGAGGATGAGGAGGACATCTGCAGGTCAAGGCCGAGCCTGAAGCTGATAGCCAGGA 315  
 Db 277 GCGAGAGGATGAGGAGGACATCTGCAGGTCAAGGCCGAGCCTGAAGCTGATAGCCAGGA 218  
 QY 316 ACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGAGATGGA 375  
 Db 217 ACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGAGATGGA 158  
 QY 376 CCGGCCAAATCCAGAGGAGTGAACCGCTGAGAGAGGTGAAGCAATCACAGTGTGA 435  
 Db 157 CCGGCCAAATCCAGAGGAGTGAACCGCTGAGAGAGGTGAAGCAATCACAGTGTGA 98  
 QY 436 AAGAAGGCGACGTTGAATGATGAGGCTGCTCCTATGTTGGAATTTGTTCAATAAAT 495  
 Db 97 AAGAAGGCGACGTTGAATGATGAGGCTGCTCCTATGTTGGAATTTGTTCAATAAAT 38  
 QY 496 TCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 532  
 Db 37 TCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 1

RESULT 8  
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 LOCUS  
 DEFINITION  
 nx15ell.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3',  
 similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.  
 AA738037  
 AA738037.1 GI:2768794  
 EST.  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 464)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Emmer-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 Cloning Distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Insert Length: 511 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 435.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP GC3"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from 3 pooled  
 germ cell tumors, and was then primed with a Not I -  
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pT7T3  
 vector. Library is not normalized. Library was  
 constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN  
 Query Match 82.7%; Score 446.8; DB 9; Length 464;  
 Best Local Similarity 98.8%; Pred. No. 2.1e-81;  
 Matches 451; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 83 ATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGTACAGCCT 142  
 Db 464 ATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGTACAGCCT 405  
 QY 143 CCTGAAATGATTTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAGTGGAAACCAACA 202  
 Db 404 CCTGAAATGATTTGGGCTATGCGGCCGAGCAGTTCAGTGATGAAGTGGAAACCAACA 345  
 QY 203 CCTGAAAGGGGAAACCAAGCACTCAACGTCAGAGTCCCTGCAGCTCTCAGGAGGAGAG 262  
 Db 344 CCTGAAAGGGGAAACCAAGCACTCAACGTCAGAGTCCCTGCAGCTCTCAGGAGGAGAG 285  
 QY 263 GATGAGGAGGACATCTGCAGGTCAAGGCCGAGCCTGAAGCTGATGCCAGGAACAGGGT 322  
 Db 284 GATGAGGAGGACATCTGCAGGTCAAGGCCGAGCCTGAAGCTGATGCCAGGAACAGGGT 225  
 QY 323 CACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGGAGATGGACCCGCA 382  
 Db 224 CACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGAGGAGATGGACCCGCA 165  
 QY 383 AATCCAGAGGAGTGAACCGCTGAGAGAGGTGAAGCAATCACAGTGTATAAAGAAG 442  
 Db 164 AATCCAGAGGAGTGAACCGCTGAGAGAGGTGAAGCAATCACAGTGTATAAAGAAG 105  
 QY 443 GCACGTTGAATGATGAGGCTGCTCCTATGTTGGAATTTGTTCAATAAATTCCTCCA 502  
 Db 104 GCACGTTGAATGATGAGGCTGCTCCTATGTTGGAATTTGTTCAATAAATTCCTCCA 45  
 QY 503 ATAAAGCTTACAGCCTTCTGCAAAAAA 540  
 Db 44 ATAAGAGTTTACAGCCTTCTGCAAAAAA 7  
 RESULT 9  
 AI381509/c  
 LOCUS  
 DEFINITION  
 te76b07.x1 Soares NFL T.GBC S1 Homo sapiens cDNA clone  
 IMAGE:2092597 3', similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;,  
 mRNA sequence.  
 AI381509  
 AI381509.1 GI:4194290  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 447)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
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/clone="IMAGE:2092597"
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/clone.lib="Soares NFL T_GBC s1"
/note="Organ: pooled; Vector: p7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NHL19W, testis NHT, and B-cell
NCI CGAP GCb1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
ORIGIN
Query Match      81.9%; Score 442.2; DB 9; Length 447;
Best Local Similarity 99.3%; Pred. No. 1.9e-80;
Matches 444; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      87  GTTCGGCAGGAGATCGACCTATTATTGGCCCTAGACCAAGCGGTATGTACAGCCTCTG 146
Db      87  |||||
QY      447 GTTCGGCAGGAGAGATCGACCTATTATTGGCCCTAGACCAAGCGGTATGTACAGCCTCTG 388
Db      447 |||||
QY      147 AAATGATTGGCCCTATGCGGCCCGAGCAGTTTCAGTGTGAAGTGAACCGACGCAACACCTG 206
Db      387 AAATGATTGGCCCTATGCGGCCCGAGCAGTTTCAGTGTGAAGTGAACCGACGCAACACCTG 328
QY      207 AAGAAGGGGAACCAAGCAACTCAAGTCAGGATCTCGAGCTGCTCAGGAGGGAGAGGATG 266
Db      327 AAGAAGGGGAACCAAGCAACTCAAGTCAGGATCTCGAGCTGCTCAGGAGGGAGAGGATG 268
QY      267 AGGAGGATCTGCAGGTCAGGGCGGAGCCTGAAGCTGATAGCCAGGAACAGGTCACC 326
Db      267 AGGAGGATCTGCAGGTCAGGGCGGAGCCTGAAGCTGATAGCCAGGAACAGGTCACC 208
QY      327 CACAGACTGGGTGTGAGTGTGAACATGGTCTCTGATGGCAGGAGATGCACCCGCCAAATC 386
Db      207 CACAGACTGGGTGTGAGTGTGAACATGGTCTCTGATGGCAGGAGATGCACCCGCCAAATC 148
QY      387 CAGAGGAGGTGAAACCCCTGAAGAAGGTGAAAAGCAATCACAGTGTATAAGAAAGGCAC 446
Db      147 CAGAGGAGGTGAAACCCCTGAAGAAGGTGAAAAGCAATCACAGTGTATAAGAAAGGCAC 88
QY      447 GTTGAATGATGAGGCTGCTCTATGTTGGAATTTGTCATTAAATTTCTCCCAATAA 506
Db      87  GTTGAATGATGAGGCTGCTCTATGTTGGAATTTGTCATTAAATTTCTCCCAATAA 28
QY      507 AGCTTTACAGCTTCTGCAAAAAA 533
Db      27  AGCTTTACAGCTTCTGCAAAAAA 1

RESULT 10
BG120336
LOCUS      BG120336
DEFINITION BG120336.1 Homo sapiens cdna clone IMAGE:4451958 5',
mRNA sequence.
ACCESSION BG120336
VERSION    BG120336.1 GI:12613845
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 480)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.

```

```

Email: cgabs-r@mail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10239 row: p column: 07
High quality sequence stop: 480.
Location/Qualifiers
1. .480
/organism="Homo sapiens"
/mcl_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4451958"
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/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."

```

Note: This is a NIH\_MSC Library.

ORIGIN	Query Match	81.2%;	Score 438.6;	DB 12;	Length 480;
	Best Local Similarity	99.1%;	Pred. No. 1e-79;		
	Matches 441;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	96	GAAGATCGACCTATTATTGGCTAGACAAGGCGCTATGTACAGCCCTCTGAAATGATG	1555		
Db	1	GAAGATCGACCTATTATTGGCTAGACAAGGCGCTATGTACAGCCCTCTGAACTGATG	60		
Qy	156	GGCCTATGCGGCCGAGCAGTTCAGTGTAGAGTGGACAGCAACACCTGAGAAAGGG	215		
Db	61	GGCCTATGCGGCCGAGCAGTTCAGTGTAGAGTGGAAACAGCAACACCTGAAAGAGGG	120		
Qy	216	AACCAACCACTCAAAGTCAGGATCCTGAGCTGCTCAGGAGGAGAGGATGAGGAGCAT	275		
Db	121	AACCAACCACTCAAAGTCAGGATCCTGAGCTGCTCAGGAGGAGAGGATGAGGAGCAT	180		
Qy	276	CTGCAGGTCAAGGGCCGAAGCGCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGACTG	335		
Db	181	CTGCAGGTCAAGGGCCGAAGCGCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGACTG	240		
Qy	336	GGTGTGAGTGTGAAGATGGTCTGTATGGCGAGGAGATGGACCCGCCAAATTCGAGAGAGG	395		
Db	241	GGTGTGAGTGTGAAGATGGTCTGTATGGCGAGGAGATGGACCCGCCAAATTCGAGAGAGG	300		
Qy	396	TGAAAACGCCCTCAAGAGGTGAAAAGCAATCACAGTGTGAAAAGAGGCAGGTGAAATG	455		
Db	301	TGAAAACGCCCTCAAGAGGTGAAAAGCAATCACAGTGTGAAAAGAGGCAGGTGAAATG	360		
Qy	456	ATGCAGGCTGCTCCTATGTTGGAAATTTGTTTCATTAAAAATTCCTCCCAATAAAGCTTTTACA	515		
Db	361	ATGCAGGCTGCTCCTATGTTGGAAATTTGTTTCATTAAAAATTCCTCCCAATAAAGCTTTTACA	420		
Qy	516	GCCCTTCTGCAAAAAAAAAAAAAAAAAA 540			
Db	421	GCCCTTCTGCAAAAAAAAAAAAAAAAAA 445			

RESULT 11	
CB115693	
LOCUS	505 bp mRNA linear EST 28-JAN-2000
DEFINITION	K-EST0159805 L8SCKO Homo sapiens cDNA clone L8SCKO-8-B09 5', mRNA sequence.
ACCESSION	CB115693
VERSION	CB115693.1 GI:27941500
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens





```

Db      150 AATCCAGAGGAGGTGAAAACGCCCTGAAGAAAGGTGAAAAGCAATCACAGTGTGTTAAAGAG 91
QY      443 GCACGTTGAAATGATCAGAGCTGCTCTATCTTGGAATTTGTTCAATAAATTTCTCCCA 502
Db      90 ACAGTTGAAATGATCAGAGCTGCTCTATCTTGGAATTTGTTCAATAAATTTCTCCCA 31
QY      503 ATAAAGCTTTACAGCCTTCTGCAAAAAA 533
Db      30 ATAAAG-TTTACAGCCTTCTGCAAAAAA 1

RESULT 13
AII187350/c
LOCUS   AII187350.1 GI:3737988
DEFINITION Homo sapiens (human)
ACCESSION AII187350
VERSION   1
KEYWORDS  EST.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 504 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 391.
Location/Qualifiers
1..455
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1751408"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NBT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer 15'
TGTACCAATCTGAAGTGGAGCGGCCGCCCAATTTTTTTTTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 77.8%; Score 420.2; DB 9; Length 455;
Best Local Similarity 97.8%; Pred. No. 6e-76;
Matches 447; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
QY      83 ATGAGTTGGCAGGAGATCGACCTATTATTGGCTAGACCAAGCGCTATGACAGCCT 142
Db      455 ATGAGTTGGCAGGAGATGACCTATTATTGGCTAGACCAAGCGCTATGACAGCCT 398
QY      143 CTTGAAATGATTGGCCCTATGCGGCCGAGCAGTTCAGTGATGAAGTGAACCAACA 202

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Db      397 CTTGAAATGATTGGCCCTATGCGGCCGAGCAGTTCAGTGATGAAGTGAACCAACA 338
QY      203 CTTGAAAGAGGGGAACAGCAACTCAACGTCAGGATCCTCGAGTCTCAGGAGGGAGAG 262
Db      337 CTTGAAAGAGGGGAACAGCAACTCAACGTCAGGATCCTCGAGTCTCAGGAGGGAGAG 278
QY      263 GATGAGGAGCATCTGAGGTCAAGGCCGAAAGCTGAAGCTGATAGCCAGGAACAGGGT 322
Db      277 GATGAGGAGCATCTGAGGTCAAGGCCGAAAGCTGAAGCTGATAGCCAGGAACAGGGT 218
QY      323 CACCCACAGACTGGGTGTGAGTGTGAAGTGTCTGATGGGCGAGAGATGGACCCCA 382
Db      217 CACCCACAGACTGGGTGTGAGTGTGAAGTGTCTGATGGGCGAGAGATGGACCCCA 158
QY      383 AATCCAGAGAGGTGAAAACGCCCTGAAGAGGTGAAAAGCAATCACAGTGTGTTAAAGAG 442
Db      157 AATCCAGAGAGGTGAAAACGCCCTGAAGAGGTGAAAAGCAATCACAGTGTGTTAAAGAG 98
QY      443 GCAGTTGAAATGATCAGGCTGCTCTATGTTGGAATTTGTTCAATAAATTTCTCCA 502
Db      97 ACAGTTGAAATGATCAGGCTGCTCTATGTTGGAATTTGTTCAATAAATTTCTCCA 38
QY      503 ATAAAGCTTTACAGCCTTCTGCAAAAAA 539
Db      37 ATAAAGCTTTACAGCCTTCTGCAAAAAA 1

RESULT 14
AII187350/c
LOCUS   AII187350.1 GI:5865303
DEFINITION Homo sapiens (human)
ACCESSION AII187350
VERSION   1
KEYWORDS  EST.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=yes.
Location/Qualifiers
1..418
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2711986"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Sub2"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI CGAP Sub2 library is a subtracted library derived from
BI. BI constitutes a mixture of 21 normalized or
subtracted NCI CGAP libraries: NCI CGAP Co4,
NCI CGAP Pr28, NCI CGAP Pr28, NCI CGAP Co10,
NCI CGAP Co16, NCI CGAP Kid5, NCI CGAP Kid12,
NCI CGAP Kid3, NCI CGAP Kid11, NCI CGAP Lym2,
NCI CGAP Br2, NCI CGAP Co8, NCI CGAP CLL1, NCI CGAP Lei2,
NCI CGAP Brn23, NCI CGAP Lu5, NCI CGAP Lu24,

```

NCI CGAP Lul9, NCI CGAP GC4, NCI CGAP GC6, NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE.CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855) NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE.CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI CGAP Lul5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE.CloneIDs 1414920-1417991, 1520904-1522439) NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE.CloneIDs 1257096-1258631, 1490064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE.CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP Col0 pool 1 LLAM 2444-2453, 2871-2872 (IMAGE.CloneIDs 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 4 million recombinants. Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches to Facilitate Gene Discovery. Genome Research 6, 791-806. TAG\_TISSUE=germ cell TAG\_LIB=NCI CGAP\_GC4 TAG\_SEQ=AAATC

## ORIGIN

Query Match 76.0%; Score 410.6; DB 9; Length 418;  
Best Local Similarity 99.0%; Pred. No. 5.6e-74;  
Matches 413; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 AAGCGCTATGTACAGCTCTCTGAAATGATGGGCTATGGCCCGCAGAGTTCAGTGA 183  
DB 418 AAGACGCTACGTAGAGCTCTCTGAAATGATGGGCTATGGCCCGCAGAGTTCAGTGA 359

QY 184 TGAAGTGAACAGCAGCAACCTGGAAGAGGGGACCAAGCACTCAACGTCAGAGTCTCTGC 243  
DB 358 TGAAGTGAACAGCAGCAACCTGGAAGAGGGGACCAAGCACTCAACGTCAGAGTCTCTGC 299

QY 244 AGCTGCTCAGAGGAGAGGATGAGGGAGCATCTGCGAGTCAAGGGCCGAAGCTGAAGC 303  
DB 298 AGCTGCTCAGAGGAGAGGATGAGGGAGCATCTGCGAGTCAAGGGCCGAAGCTGAAGC 239

QY 304 TGATAGCCAGCAAGAGGCTCACCCACAGCTGGGTGTCAGTGTGAAGTGTCTCTGATGG 363  
DB 238 TCATAGCCAGCAAGAGGCTCACCCACAGCTGGGTGTCAGTGTGAAGTGTCTCTGATGG 179

QY 364 GCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGGCTGAAGAGGCTGAAGCA 423  
DB 178 GCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGGCTGAAGAGGCTGAAGCA 119

QY 424 ATCAGAGTGTAAAGAGAGCAGTGTGAATGATGCGAGGCTGCTCTATGTTGGAATTT 483  
DB 118 ATCAGAGTGTAAAGAGAGCAGTGTGAATGATGCGAGGCTGCTCTATGTTGGAATTT 59

QY 484 GTTCATTTAAATCTCCCAATAAGCTTTACAGCTCTCTGCAAAAAAATAAAAAA 540  
DB 58 GTTCATTTAAATCTCCCAATAAGCTTTACAGCTCTCTGCAAAAAAATAAAAAA 2

RESULT 15  
AA868226/c  
LOCUS  
DEFINITION  
ak49h07.s1 Soares testis Nhr Homo sapiens cdna clone IMAGE:1409245  
3', similar to SW:GGE2\_HUMAN Q13066 GAGE-2 PROTEIN. [1] ;, mRNA  
sequence.  
ACCESSION  
AA868226.1 GI:2963671  
VERSION  
AA868226  
KEYWORDS  
EST.  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 426)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
cdna Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cdna Library Arrayed by: Greg Lennon, Ph.D.  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Possible reversed clone: similarity on wrong strand  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 363.

## FEATURES

Location/Qualifiers  
source  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1409245"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/notes="Vector: pT7T3D-Pac-(Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cdna  
was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5].  
TGTTACCAATCTGAAGTGGAGGGCGCGCCCAATTTTTTTTTTTT 3']  
Double-stranded cdna was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 74.4%; Score 402; DB 9; Length 426;  
Best Local Similarity 97.1%; Pred. No. 3.2e-72;  
Matches 408; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 110 TATTGGCTACACCAAGCGCTATGTACAGCTCTCTGAAATGATTTGGCGCTATGCGGCC 169  
DB 420 TATCGGCTAGACCAAGCGCTAGTAGAGCTCTCTGAAATGNANTTGCCTATGCGGCC 361

QY 170 GAGCAGTTCAGTGTAGTGAACCCAGCAACACCTGAAGAGGGGAACCAAGCACTCAA 229  
DB 360 GAGCAGTTCAGTGTAGTGAACCCAGCAACACCTGAAGAGGGGAACCAAGCACTCAA 301

QY 230 CGTCAGATCTCGAGCTGCTCAGAGGGAGAGTGAAGGAGCATCTGCAAGTCAAGGG 289  
DB 300 CGTCAGATCTCGAGCTGCTCAGAGGGAGAGTGAAGGAGCATCTGCAAGTCAAGGG 241

QY 290 CCGAAGCTCTGAAGCTGTAGCCAGAACAGGGTCAACCACAGACTGGGTGTGAGTGTCAA 349  
DB 240 CCGAAGCTCTGAAGCTGTAGCCAGAACAGGGTCAACCACAGACTGGGTGTGAGTGTCAA 181

QY 350 GATGCTCTGTATGGCGAGGATGACCCGCCAAATCCAGAGGAGGTGAACACGCTCAA 409  
DB 180 GATGCTCTGTATGGCGAGGATGACCCGCCAAATCCAGAGGAGGTGAACACGCTCAA 121

QY 410 GAAGGTGAAGACCATCACAGTGTAAAGAGGACGCTTCAATATGATGCGAGGCTGCTCC 469  
DB 120 GAAGGTGAAGACCATCACAGTGTAAAGAGGACGCTTCAATATGATGCGAGGCTGCTCC 61

QY 470 TATGTTGAAATTTTGTTCATTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAAA 529  
DB 60 TATGTTGAAATTTTGTTCATTAATAATCTCCCAATAAGCTTTACAGCTTCTTCAAAA 1

Search completed: August 6, 2004, 18:20:17  
Job time : 2420 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 13:00:38 ; Search time 329 Seconds  
(without alignments)  
6972.726 Million cell updates/sec

Title: US-09-782-745-16

Perfect score: 540

Sequence: 1 CGCCAGGAGCTGTGAGGCA.....CTGCAAAAAAAAAAAAAA 540

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5025714

Minimum DB seq length: 0

Maximum DB seq length: 540

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	540	100.0	540	2	AAX90521
2	534.2	98.9	540	2	AAX90523
3	528.8	97.9	532	2	AAX90522
4	528	97.8	528	6	ABL66323
5	524.6	97.1	539	2	AAV18721
6	522.2	96.7	527	7	ACC51027
7	522.2	96.7	527	7	ABX76236
8	520.8	96.4	532	2	AAV18720
9	512.8	95.0	538	2	AAX90519
10	508.8	94.2	526	7	ADAI5802
11	504.8	93.5	530	7	ADAI5801
12	504.4	93.4	528	7	ADAI5801
13	471	87.2	535	2	AAV18717
14	360.4	66.7	430	3	AAO2129
15	306.2	56.7	530	4	AAO2129
16	304	56.3	365	4	AAO2129
17	245	45.4	257	7	ABZ19555
18	245	45.4	264	7	ABZ19555
19	243.4	45.1	277	7	ABZ19551
20	229	42.4	229	7	ABZ20497
21	225.4	41.7	227	7	ABZ20480
22	224.4	41.6	229	7	ABZ18686
23	221	40.9	259	7	ABZ19791

24	210	38.9	520	7	ABT15737	Abt15737 Human can
25	205.6	38.1	225	7	ABZ19533	Abz19533 Group III
26	202.4	37.5	509	7	ABX77605	Abx77605 Different
27	202.4	37.5	509	8	ACD42232	Acad42232 Human GAG
28	202.4	37.5	509	9	ADC24646	Adc24646 Human GAG
29	187	34.6	532	4	AAI60530	Aai60530 Human pol
30	180.6	33.4	219	7	ABZ19538	Abz19538 Group III
31	164.2	30.4	503	5	AAS69484	Aas69484 DNA encod
32	141.6	26.2	528	7	ABT15728	Abt15728 Human can
33	131.6	24.4	475	4	AAD14981	Aad14981 Human can
34	126.6	23.4	538	7	ABT15736	Abt15736 Human can
35	109.6	20.3	399	5	AAF68151	Aaf68151 Human lun
36	109.6	20.3	399	6	ABK38062	Abk38062 cDNA enco
37	109.6	20.3	399	7	ACA10391	Aca10391 Human lun
38	109.6	20.3	399	7	ABX99342	Abx99342 Lung can
39	109.6	20.3	399	10	ADP72125	Adp72125 Human lun
40	105.2	19.5	505	6	AAD24228	Aad24228 Human dif
41	105	19.4	463	6	ABA92217	Aba92217 Melanoma
42	103.2	19.1	515	4	AAH93807	Aah93807 Human pro
43	103.2	19.1	515	4	AAS63900	Aas63900 Human pro
44	103.2	19.1	515	4	AAH02872	Aah02872 Prostate
45	103.2	19.1	515	4	AAH85121	Aah85121 Human pro

## ALIGNMENTS

RESULT 1  
AAX90521  
ID AAX90521 standard; cDNA; 540 BP.  
XX  
AC AAX90521;  
XX  
DT 30-SEP-1999 (first entry)  
XX  
DE GAGE-4 tumour rejection antigen clone nucleotide sequence.  
XX  
KW Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
KW GAGE; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9937665-Al.  
XX  
PD 29-JUL-1999.  
XX  
PF 12-JAN-1999; 99WO-US000775.  
XX  
PR 23-JAN-1998; 98US-00012818.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;  
XX  
DR WPI; 1999-469111/39.  
XX  
PT New isolated peptides which bind to HLA-A29 molecules, which are tumor  
PT rejection antigens used for detection and therapy of pathological  
XX conditions, e.g. cancer.  
XX  
PS Example 13; Fig 4; 62pp; English.  
XX  
CC The present invention describes peptides which bind to human leukocyte  
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into  
CC tumour rejection antigens. They can be used for detecting cytolytic T  
CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-  
CC typing assays. Complexes of HLA-29 molecules and the peptides can be used  
CC for stimulating CTLs in vivo. The present sequence represents a GAGE  
CC tumour rejection antigen clone, from an example from the present  
XX invention  
SQ Sequence 540 BP; 159 A; 114 C; 156 G; 111 T; 0 U; 0 Other;

```
PT rejection antigens used for detection and therapy of pathological
PT conditions, e.g. cancer.
XX Example 13; Fig 4; 62pp; English.
PS
XX
XX The present invention describes peptides which bind to human leukocyte
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into
CC tumour rejection antigens. They can be used for detecting cytolytic T
CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-
CC typing assays. Complexes of HLA-29 molecules and the peptides can be used
CC for stimulating CTLs in vivo. The present sequence represents a GAGE
CC tumour rejection antigen clone, from an example from the present
CC invention
XX
SQ Sequence 540 BP; 159 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
Query Match 98.9%; Score 534.2; DB 2; Length 540;
Best Local Similarity 99.4%; Pred. No. 7.7e-143;
Matches 536; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GCACAGGAGCTGTGAGGAGCTGTGTGTGTCTCTGCGTCCGACCTCTTTTCTCTAC 61
Db 1 GCACAGGAGCTGTGAGGAGCTGTGTGTGTCTCTGCGTCCGACCTCTTTTCTCTAC 60
QY 62 TGAGATTCACTCTGTGAAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGA 121
Db 61 TGAGATTCACTCTGTGAAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGA 120
QY 122 CCAAGGCGCTATGTACAGCCTCTCTGAAATCATTTGGGCTATGCGGCCGAGCAGTTCACT 181
Db 121 CCAAGGCGCTATGTACAGCCTCTCTGAAATCATTTGGGCTATGCGGCCGAGCAGTTCACT 180
QY 182 GATGAAGTGGAAACAGCAACACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGATCCT 241
Db 181 GATGAAGTGGAAACAGCAACACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGATCCT 240
QY 242 GCAGCTGCTCAGGAGGAGAGGATGAGGAGCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 301
Db 241 GCAGCTGCTCAGGAGGAGAGGATGAGGAGCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 300
QY 302 GCTGATAGCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 361
Db 301 GCTGATAGCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 360
QY 362 GGGCAGGAGATGAGACCCGCCAAATCCAGAGGAGTGAACCGCTGAAAGAGGTGAAGAAG 421
Db 361 GGGCAGGAGATGAGACCCGCCAAATCCAGAGGAGTGAACCGCTGAAAGAGGTGAAGAAG 420
QY 422 CAATCAGAGTGTAAAGAGGAGGAGTGAATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 481
Db 421 CAATCAGAGTGTAAAGAGGAGGAGTGAATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 480
QY 482 TTGTTTCAATAAATTTCTCCCAATAAAGCTTTTACAGCCTTTCTGCAAAAAA 540
Db 481 TTGTTTCAATAAATTTCTCCCAATAAAGCTTTTACAGCCTTTCTGCAAAAAA 539

RESULT 3
AAAX90522
ID AAAX90522 standard; cDNA; 532 BP.
XX
XX AC AAAX90522;
XX
XX 30-SEP-1999 (first entry)
XX
XX GAGE-5 tumour rejection antigen clone nucleotide sequence.
XX
XX Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;
XX therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;
XX GAGE; ss.
XX
XX Homo sapiens.
XX
```

```
Query Match 100.0%; Score 540; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.7e-144;
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCAGGAGCTGTGAGGAGCTGTGTGTGTCTCTGCGTCCGACCTCTTTTCTCTCTA 60
Db 1 CGCAGGAGCTGTGAGGAGCTGTGTGTGTCTCTGCGTCCGACCTCTTTTCTCTCTA 60
QY 61 CTGAGATTCACTCTGTGAAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAG 120
Db 61 CTGAGATTCACTCTGTGAAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAG 120
QY 121 ACCAAGCGCTATGTACAGCCTCTCTGAAATGATTTGGGCTATGCGGCCGAGAGTTTCA 180
Db 121 ACCAAGCGCTATGTACAGCCTCTCTGAAATGATTTGGGCTATGCGGCCGAGAGTTTCA 180
QY 181 TGATGAAGTGAACCAACACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGATCC 240
Db 181 TGATGAAGTGAACCAACACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGATCC 240
QY 241 TGCAGCTGCTCAGGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGCGCGAGAGCTGA 300
Db 241 TGCAGCTGCTCAGGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGCGCGAGAGCTGA 300
QY 301 AGCTGATAGCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAGTGTGAGTGTGAGT 360
Db 301 AGCTGATAGCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAGTGTGAGTGTGAGT 360
QY 361 TGGCAGGAGATGACCGCCCAATCCAGAGGAGTGAACCGCTGAAAGAGGTGAAGA 420
Db 361 TGGCAGGAGATGACCGCCCAATCCAGAGGAGTGAACCGCTGAAAGAGGTGAAGA 420
QY 421 GCAATCAGAGTGTAAAGAGAGGACGTTGAAATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGT 480
Db 421 GCAATCAGAGTGTAAAGAGAGGACGTTGAAATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGT 480
QY 481 TTTGTTTCAATAAATTTCTCCCAATAAAGCTTTTACAGCCTTTCTGCAAAAAA 540
Db 481 TTTGTTTCAATAAATTTCTCCCAATAAAGCTTTTACAGCCTTTCTGCAAAAAA 540

RESULT 2
AAAX90523
ID AAAX90523 standard; cDNA; 540 BP.
XX
XX AC AAAX90523;
XX
XX 30-SEP-1999 (first entry)
XX
XX GAGE-6 tumour rejection antigen clone nucleotide sequence.
XX
XX Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;
XX therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;
XX GAGE; ss.
XX
XX Homo sapiens.
XX
XX WO9937665-A1.
XX
XX 29-JUL-1999.
XX
XX 12-JAN-1999; 99WO-US000775.
XX
XX 23-JAN-1998; 98US-00012818.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;
XX WPI; 1999-469111/39.
XX
XX New isolated peptides which bind to HLA-A29 molecules, which are tumor
```

PN WO9937665-A1.  
XX 29-JUL-1999.  
XX 12-JAN-1999; 99WO-US000775.  
XX 23-JAN-1998; 98US-00012818.  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;  
XX WPI; 1999-469111/39.  
XX New isolated peptides which bind to HLA-A29 molecules, which are tumor  
PT rejection antigens used for detection and therapy of pathological  
PT conditions, e.g. cancer.  
XX  
XX Example 13; Fig 4; 62pp; English.  
XX The present invention describes peptides which bind to human leukocyte  
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into  
CC tumor rejection antigens. They can be used for detecting cytolytic T  
CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-  
CC typing assays. Complexes of HLA-29 molecules and the peptides can be used  
CC for stimulating CTLs in vivo. The present sequence represents a GAGE  
CC tumour rejection antigen clone, from an example from the present  
CC invention  
XX  
XX Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 U; 0 Other;  
Query Match 97.9%; Score 528.8; DB 2; Length 532;  
Best Local Similarity 99.6%; Pred. No. 2.7e-141;  
Matches 530; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 9 AGCTGTGAGGAGTGTGTGTGTTCTCGCTCGGACTCTTTTCTCTACTGAGATT 68  
Db 1 AGCTGTGAGGAGTGTGTGTGTTCTCGCTCGGACTCTTTTCTCTACTGAGATT 60  
OY 69 CATCTGTGAAATATGATGGCGAGGAGATGCACTTATTATGGGCTAGCAAGGC 128  
Db 61 CATCTGTGAAATATGATGGCGAGGAGATGCACTTATTATGGGCTAGCAAGGC 120  
OY 129 GCTATGTACAGCTCTGAAATGATTGGCCCTATGGCCCGGAGTTCAGTGTGATGA 188  
Db 121 GCTATGTACAGCTCTGAAATGATTGGCCCTATGGCCCGGAGTTCAGTGTGATGA 180  
OY 189 TGGAAACCCAGCACTCTGAAAGAGGGGAACCAAGCACTCAAGTCAGGATCCTGAGCTG 248  
Db 181 TGGAAACCCAGCACTCTGAAAGAGGGGAACCAAGCACTCAAGTCAGGATCCTGAGCTG 240  
OY 249 CTCAGAGGGAGAGATGAGGAGCAATCTGCAAGTCAAGGCGGAAGCTGAAGCTGATA 308  
Db 241 CTCAGAGGGAGAGATGAGGAGCAATCTGCAAGTCAAGGCGGAAGCTGAAGCTGATA 300  
OY 309 GCGAGGAACAGGTCACCCACAGACTGGTGTGAGTGAAGTGGTCTGTGATGGGCGAG 368  
Db 301 GCGAGGAACAGGTCACCCACAGACTGGTGTGAGTGAAGTGGTCTGTGATGGGCGAG 360  
OY 369 AGATGACCCGCAATCCAGAGGAGGTGAAACGCTCAAGAAAGTGAAGCAATCAC 428  
Db 361 AGATGACCCGCAATCCAGAGGAGGTGAAACGCTCAAGAAAGTGAAGCAATCAC 420  
OY 429 AGTGTAAAGAGGACGTTGAAATGATGCGAGGCTGCTCTATGTGGAATTTGTCA 488  
Db 421 AGTGTAAAGAGGACGTTGAAATGATGCGAGGCTGCTCTATGTGGAATTTGTCA 480  
OY 489 TTAATAATCTCCCAATAGCTTTACAGCCTTCTGCAAAAAA 540  
Db 481 TTAATAATCTCCCAATAGCTTTACAGCCTTCTGCAAAAAA 532  
RESULT 4

ABL66323  
ID ABL66323 standard; DNA; 528 BP.  
XX  
AC ABL66323;  
XX  
DT 15-MAY-2002 (first entry)  
XX  
DE Lung cancer related gene sequence SEQ ID NO:4660.  
XX  
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200194629-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 30-MAY-2001; 2001WO-US010838.  
XX  
PR 05-JUN-2000; 2000US-0209473P.  
PR 05-JUN-2000; 2000US-0209531P.  
PR 18-SEP-2000; 2000US-023313P.  
PR 18-SEP-2000; 2000US-0233617P.  
PR 20-SEP-2000; 2000US-0234009P.  
PR 20-SEP-2000; 2000US-0234034P.  
PR 20-SEP-2000; 2000US-0234052P.  
PR 22-SEP-2000; 2000US-0234509P.  
PR 22-SEP-2000; 2000US-0234567P.  
PR 25-SEP-2000; 2000US-0234923P.  
PR 25-SEP-2000; 2000US-0234924P.  
PR 25-SEP-2000; 2000US-0235077P.  
PR 25-SEP-2000; 2000US-0235082P.  
PR 25-SEP-2000; 2000US-0235134P.  
PR 26-SEP-2000; 2000US-0235280P.  
PR 26-SEP-2000; 2000US-0235637P.  
PR 26-SEP-2000; 2000US-0235638P.  
PR 27-SEP-2000; 2000US-0235711P.  
PR 27-SEP-2000; 2000US-0235720P.  
PR 27-SEP-2000; 2000US-0235840P.  
PR 27-SEP-2000; 2000US-0235863P.  
PR 28-SEP-2000; 2000US-0236028P.  
PR 28-SEP-2000; 2000US-0236032P.  
PR 28-SEP-2000; 2000US-0236033P.  
PR 28-SEP-2000; 2000US-0236034P.  
PR 28-SEP-2000; 2000US-0236109P.  
PR 29-SEP-2000; 2000US-0236111P.  
PR 29-SEP-2000; 2000US-0236842P.  
PR 29-SEP-2000; 2000US-0236891P.  
PR 02-OCT-2000; 2000US-0237172P.  
PR 02-OCT-2000; 2000US-0237173P.  
PR 02-OCT-2000; 2000US-0237278P.  
PR 02-OCT-2000; 2000US-0237294P.  
PR 02-OCT-2000; 2000US-0237295P.  
PR 02-OCT-2000; 2000US-0237316P.  
PR 03-OCT-2000; 2000US-0237425P.  
PR 03-OCT-2000; 2000US-0237598P.  
PR 03-OCT-2000; 2000US-0237604P.  
PR 03-OCT-2000; 2000US-0237606P.  
PR 03-OCT-2000; 2000US-0237608P.  
PR 01-NOV-2000; 2000US-0244867P.  
PR 01-NOV-2000; 2000US-0245084P.  
XX  
XX (AVAL-) AVALON PHARM.  
XX  
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
PI Soppet DR, Weaver Z;  
XX  
XX WPI; 2002-188264/24.  
XX  
XX Screening for anti-neoplastic agent involves exposing cells to a chemical

PT agent to be tested for anti-neoplastic activity, and determining a change  
 PT in expression of a gene of a signature gene set.

PS Claim 1; SEQ ID NO 4660; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-  
 CC neoplastic agent. The method involves exposing cells to a chemical agent  
 CC to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in ABU61664  
 CC to ABU70110), or is at least 95% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening an  
 CC anti-neoplastic agent, and can be used for producing a product which is  
 CC the data collected with respect to the anti-neoplastic agent as a result  
 CC of M1, and the data is sufficient to convey the chemical structure and/or  
 CC properties of the agent. M1 can be used in the treatment of cancer such  
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms's  
 CC tumour

XX SQ Sequence 528 BP; 147 A; 114 C; 156 G; 111 T; 0 U; 0 Other;

Query Match 97.8%; Score 528; DB 6; Length 528;

Best Local Similarity 100.0%; Pred. No. 4.5e-141; Length 528;

Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCAGGAGGAGTGTGAGGCAAGTGTGTGTCTTCCCGTCCGGACTCTTTTCCCTCA 60

Db 1 CGCCAGGAGGAGTGTGAGGCAAGTGTGTGTCTTCCCGTCCGGACTCTTTTCCCTCA 60

Qy 61 CTGAGATTCATCTGTGTAATATGATGTGGCGAGGAGATCGACCTATTATTGGCCCTAG 120

Db 61 CTGAGATTCATCTGTGTAATATGATGTGGCGAGGAGATCGACCTATTATTGGCCCTAG 120

Qy 121 ACCAAGCGCTATGTACAGCTCTCTGAAATGATTGGGCGCTATGGCGCCGAGCAGTTTCAG 180

Db 121 ACCAAGCGCTATGTACAGCTCTCTGAAATGATTGGGCGCTATGGCGCCGAGCAGTTTCAG 180

Qy 181 TGATGAAGTGAACACAGCAACACCTGAAGAGGGGAAACCACTCAAGTCAGATCC 240

Db 181 TGATGAAGTGAACACAGCAACACCTGAAGAGGGGAAACCACTCAAGTCAGATCC 240

Qy 241 TGCAGCTGCTCAGAGGAGGAGTGGGAGCATCTGCAGTCAAGGCGCGAGCCTGA 300

Db 241 TGCAGCTGCTCAGAGGAGGAGTGGGAGCATCTGCAGTCAAGGCGCGAGCCTGA 300

Qy 301 AGCTGATAGCCAGGAACAGGCTACCCACAGACTGGGTGTGAGTGTCAAGATGTCCTGA 360

Db 301 AGCTGATAGCCAGGAACAGGCTACCCACAGACTGGGTGTGAGTGTCAAGATGTCCTGA 360

Qy 361 TGGCAGAGATGAGACCGCCCAATCCAGAGAGGTGAACCGCTGAAGAGGTGAAAA 420

Db 361 TGGCAGAGATGAGACCGCCCAATCCAGAGAGGTGAACCGCTGAAGAGGTGAAAA 420

Qy 421 GCATACAGTGTAAAGAGGACGTTGAATGATGACGCTGCTCTATGTTGAAA 480

Db 421 GCATACAGTGTAAAGAGGACGTTGAATGATGACGCTGCTCTATGTTGAAA 480

Qy 481 TTTGTTTCAAAAATTTCCCAATAAAGCTTTTACAGCTTCTGCAAAA 528

Db 481 TTTGTTTCAAAAATTTCCCAATAAAGCTTTTACAGCTTCTGCAAAA 528

RESULT 5

AAV18721

XX AAV18721 standard; cDNA; 539 BP.

AC AAV18721;

XX 30-JUL-1998 (first entry)

DT

XX cDNA encoding GAGE-6 tumour rejection antigen precursor.

XX GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;

KW melanoma; antigen; cytolytic T cell clone proliferation;

KW HLA-typing assay; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

CDS 82..436

FT /tag= a

FT /transl\_except= (pos:127..129, aa:Arg)

FT /transl\_except= (pos:196..198, aa:Ala)

FT /transl\_except= (pos:199..201, aa:Thr)

XX MO9749417-A1.

XX 31-DEC-1997.

XX 23-JUN-1997; 97WC-US010850.

XX 24-JUN-1996; 96US-00669161.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Debacker O, Van Den Bynde B, Boon-Falleur T;

XX WPI; 1998-076905/07.

XX P-PSDB; AAW47603.

XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -

XX processed by HLA-Cw6 molecules into peptides, useful to diagnose

XX melanomas.

XX Example 13; Fig 4; 60pp; English.

XX The present sequence encodes a GAGE-6 tumour rejection antigen

XX precursor (TRAP). The protein is expressed in a number of tumours. In

XX contrast the only normal tissue which expresses GAGE TRAP protein is

XX testis. Several GAGE TRAPs have been identified (see AAV18717-21). The

XX major difference between these proteins and GAGE-1 (AAV05540) is the

XX absence of a stretch of 143 bases located at position 379 to 521 of the

XX GAGE-1 TRAP sequence. The rest of the sequences show mismatches at

XX various position, with the exception of GAGE-3 whose 5' end is totally

XX different from the other GAGE cDNAs for the first 112 bases. This region

XX of GAGE-3 cDNA contains a long repeat and a hairpin structure. The

XX antigens can be used to diagnose melanomas, characterised by expression

XX of a TRAP or presentation of a tumour rejection antigen. Antigens shed

XX into blood or urine can be observed and then used to confirm a diagnosis

XX of melanoma using cytolytic T cell clone proliferation methodologies.

XX Other uses for the processed peptides, include HLA-typing assays for,

XX e.g. skin graft or organ transplants

XX SQ Sequence 539 BP; 157 A; 114 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 97.1%; Score 524.6; DB 2; Length 539;

Best Local Similarity 98.3%; Pred. No. 4.4e-140;

Matches 530; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GCACGGAGCTGTGAGGACAGTGTGTGTGTTCTGCGCTCCGAGCTCTTTTCTCTAC 61

Db 1 GCCAGGAGCTGTGAGGACAGTGTGTGTGTTCTGCGCTCCGAGCTCTTTTCTCTAC 60

Qy 62 TGAGATTCATCTGTGTAATATGAGTGGGAGAGATCGACTATTATGGCCTAGA 121

Db 61 TGAGATTCATCTGTGTAATATGAGTGGGAGAGATCGACTATTATGGCCTAGA 120

Qy 122 CCAAGGCGCTATGTACAGCCTCTCTGAAATGATTGGGCTATGCGGCCGAGCAGTTCACT 181

Db 121 CCAAGGCGCTATGTACAGCCTCTCTGAAATGATTGGGCTATGCGGCCGAGCAGTTCACT 180

Qy 182 GATGAAGTGAACACAGCAACACCTGAAGAGGGGAAACCACTCAACGTCAGATCCT 241



Db 181 GATGAAGTGAACACAGAGCTCTCTGAAGAGGGGAACCAACCACTCAAGTCAGGATCCT 240  
QY 242 GCAGCTGCTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAA 301  
Db 241 GCAGCTGCTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAA 300  
QY 302 GCTGATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 361  
Db 301 GCTGATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 360  
QY 362 GGGCAGAGATGACCCCGCCAAATCCAGAGGAGGTGAAGACGCTGAAGAGGTGAAAAG 421  
Db 361 GGGCAGAGGTGACCCCGCCAAATCCAGAGGAGGTGAAGACGCTGAAGAGGTGAAAAG 420  
QY 422 CAATCAGCTGTTAAAGAGGACCGTGAAGATGATGAGGCTGCTCTATGTTGGAAT 481  
Db 421 CAATCAGCTGTTAAAGAGGACCGTGAAGATGATGAGGCTGCTCTATGTTGGAAT 480  
QY 482 TTGTTTCAATTAATAATTCCTCAATAAGCTTTACAGCTTCTGCAAAAAA 540  
Db 481 TTGTTTCAATTAATAATTCCTCAATAAGCTTTACAGCTTCTGCAAAAAA 539

RESULT 6  
ACCS1027  
ID ACCS1027 standard; cdna; 527 BP.

XX  
AC ACCS1027;  
XX  
DT 12-JUN-2003 (first entry)

XX Human bladder cancer associated cdna sequence SEQ ID NO:144.

DE Human bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.

XX Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.

XX Homo sapiens.

XX W02003003906-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US021338.

XX 03-JUL-2001; 2001US-0302814P.

XX 03-AUG-2001; 2001US-0310099P.

XX 08-NOV-2001; 2001US-0343705P.

XX 13-NOV-2001; 2001US-0350666P.

XX 12-APR-2002; 2002US-0372246P.

XX (ECOB-) EOS BIOTECHNOLOGY INC.

XX Mack DH, Aziz N;

XX WPI; 2003-201532/19.

XX P-PSDB; ABR48213.

XX Detecting a bladder cancer-associated transcript in a cell from a

XX patient, comprises contacting a biological sample from the patient with a

XX bladder cancer-associated polynucleotide or antibody.

XX Claim 6; Page 279; 307pp; English.

XX The present invention describes a method for detecting a bladder cancer-

XX associated transcript in a cell from a patient. The method comprises

XX contacting a biological sample from the patient with a polynucleotide

XX that selectively hybridises to a sequence that is 80 % identical to a

XX table of sequences (see ACCS0951 to ACCS1059). ACCS0951 to ACCS1059

XX encode the human bladder cancer-associated proteins given in ABR48146 to

XX ABR48242). Bladder cancer-associated sequences from the present invention

XX have cytostatic activities, and can be used in antisense gene therapy and

XX in vaccine production. The method can be used for detecting a bladder

XX cancer-associated transcript in a cell from a patient. The method is

CC useful in diagnosing or treating bladder cancer and in screening for  
CC compounds that modulate bladder cancer, such as hormones or antibodies.  
CC The nucleic acid molecules from the present invention may be used in  
CC various screening and diagnostic methods, and for gene therapy, vaccine  
CC and/or antisense/inhibition applications

XX  
SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 96.7%; Score 522.2; DB 7; Length 527;

Best Local Similarity 99.4%; Pred. No. 2.1e-139;

Matches 524; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCAGGGAGCTGTGAGGAGTCTGTGTCTCTCGCTCGGTCGCGACTCTTTTCTCTAC 61

Db 1 GCAGGGAGCTGTGAGGAGTCTGTGTCTCTCGCTCGGACTCTTTTCTCTAC 60

QY 62 TGAGATTTCATCTGTGTGAATATGAGTTGGCAGGAAGATCGACCTATTATTGGCCTAGA 121

Db 61 TGAGATTTCATCTGTGTGAATATGAGTTGGCAGGAAGATCGACCTATTATTGGCCTAGA 120

QY 122 CMAGGGCTATGTACAGCTCTCTGAATGATTTGGGCTTATCGGCGCCGAGAGTTCAGT 181

Db 121 CCAAGGGCTATGTACAGCTCTCTGAATGATTTGGGCTTATCGGCGCCGAGAGTTCAGT 180

QY 182 GATGAAGTGGAAACAGCAACACCTGAAGAGGGGAACCACTCAACGTCAGGATCCT 241

Db 181 GATGAAGTGGAAACAGCAACACCTGAAGAGGGGAACCACTCAACGTCAGGATCCT 240

QY 242 GCAGCTGCTCAGGAGGAGGAGTGAAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAA 301

Db 241 GCAGCTGCTCAGGAGGAGGAGTGAAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAA 300

QY 302 GCTGATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGTGTCTGAT 361

Db 301 GCTGATAGCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGTGTCTGAT 360

QY 362 GGGCAGGAGTGGACCCGCCAAATCCAGAGGAGGTGAAGACGCTGAAGAGGTGAAAAG 421

Db 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGGAGGTGAAGACGCTGAAGAGGTGAAAAG 420

QY 422 CAATCAGTGTGTTAAAGAGGACCGTGTGAATGATGCAGGCTGCTCTATGTTGGAAT 481

Db 421 CAATCAGTGTGTTAAAGAGGACCGTGTGAATGATGCAGGCTGCTCTATGTTGGAAT 480

QY 482 TTGTTTCAATTAATAATTCCTCAATAAGCTTTACAGCTTCTGCAAAA 528

Db 481 TTGTTTCAATTAATAATTCCTCAATAAGCTTTACAGCTTCTGCAAAA 527

RESULT 7

ABX76236

ID ABX76236 standard; DNA; 527 BP.

XX  
AC ABX76236;

XX  
DT 02-APR-2003 (first entry)

XX Lung cancer-associated polynucleotide #105.

XX Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;

XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;

XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX W0200286443-A2.

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US012476.

XX

PR 18-APR-2001; 2001US-0284770P.  
 PR 10-MAY-2001; 2001US-0290492P.  
 PR 09-NOV-2001; 2001US-0339245P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 29-NOV-2001; 2001US-0334370P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Aziz N, Murray R;  
 XX  
 DR WPI: 2003-093161/08.  
 DR P-PSDB; ABUS6512.  
 XX  
 PT Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer.  
 XX  
 PS Claim 22; Page 273; 453pp; English.  
 XX  
 CC The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridises  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung cancer-  
 CC associated polynucleotides and polypeptides are used for identifying a  
 CC compound that modulates a lung cancer-associated polypeptide, for  
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
 CC cancer in a patient and for treating a mammal having lung cancer by  
 CC administering a modulatory compound identified. The methods are useful  
 CC for treating lung cancer, such as small cell lung cancer, non-small cell  
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
 CC for diagnostic purposes and as targets for screening for therapeutic  
 CC compounds that modulate lung cancer, such as antibodies. Sequences  
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the  
 CC invention  
 XX  
 SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 96.7%; Score 522.2; DB 7; Length 527;  
 Best Local Similarity 99.4%; Pred. No. 2.1e-139;  
 Matches 524; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 2 GCCAGGAGCTGTGAGGAGTGTCTGTGTCTCTGCGTCCGACTCTTTTCTCTAC 61  
 DB 1 GCCAGGAGCTGTGAGGAGTGTCTGTGTCTCTGCGTCCGACTCTTTTCTCTAC 60  
 OY 62 TGAGATTCTCTGTGAAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGA 121  
 DB 61 TGAGATTCTCTGTGAAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGA 120  
 OY 122 CCAAGGCCATATGACACCTCTGAAATGATGTTGGCTATGCGGCCGAGAGTTCACT 181  
 DB 121 CCAAGGCCATATGACACCTCTGAAATGATGTTGGCTATGCGGCCGAGAGTTCACT 180  
 OY 182 GATGAAGTGGAAACCAAGCAACCTGAAAGGGGAAACCAAGCACTCAACGTCAGATCCT 241  
 DB 181 GATGAAGTGGAAACCAAGCAACCTGAAAGGGGAAACCAAGCACTCAACGTCAGATCCT 240  
 OY 242 GCAGTGTCTAGGAGGAGAGATGAGGAGCATCTGAGGTCAGAGTCAAGGCCGAGCCTGAA 301  
 DB 241 GCAGTGTCTAGGAGGAGAGATGAGGAGCATCTGAGGTCAGAGTCAAGGCCGAGCCTGAA 300  
 OY 302 GCTGATAGCCAGGACAGGTCACCCAGAGTGGTGTGAGTGTGAAGATGCTCTGAT 361  
 DB 301 GCTGATAGCCAGGACAGGTCACCCAGAGTGGTGTGAGTGTGAAGATGCTCTGAT 360  
 OY 362 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGTGAACCGCTCGAAGAGGTGAAAG 421

DB 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGGAGTGAACCGCTCGAAGAGGTGAAAG 420  
 OY 422 CAATCACAGTGTAAAGAGGACGCTTCAATATGATGAGGCTGCTCTATCTTGAAT 481  
 DB 421 CAATCACAGTGTAAAGAGGACGCTTCAATATGATGAGGCTGCTCTATCTTGAAT 480  
 OY 482 TTGTTTCATTAATAATCTCCCAATAAAGCTTTACAGCTTCTGCAAAA 528  
 DB 481 TTGTTTCATTAATAATCTCCCAATAAAGCTTTACAGCTTCTGCAAAA 527

# RESULT 8

AAV18720  
 ID AAV18720 standard; cDNA; 532 BP.  
 XX  
 AC AAV18720;  
 XX  
 DT 30-JUL-1998 (first entry)  
 XX  
 DE cDNA encoding GAGE-5 tumour rejection antigen precursor.  
 XX  
 KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;  
 KW melanoma; antigen; cytolytic T cell clone proliferation;  
 KW HLA-typing assay; ss.  
 XX  
 OS Homo sapiens.  
 EH Key Location/Qualifiers  
 FT CDS 75..429  
 FT /\*tag= a  
 FT /transl\_except= (pos:189..191, aa:Ala)  
 FT /transl\_except= (pos:192..194, aa:Thr)  
 XX  
 PN WO9749417-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 23-JUN-1997; 97WO-US010850.  
 XX  
 PR 24-JUN-1996; 96US-00669161.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Debacker O, Van Den Eynde B, Boon-Falleur T;  
 XX  
 DR WPI: 1998-076905/07.  
 DR P-PSDB; AAW47602.  
 XX  
 PT Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -  
 PT processed by HLA-Cw6 molecules into peptides, useful to diagnose  
 PT melanomas.  
 XX  
 PS Example 13; Fig 4; 60pp; English.  
 XX  
 CC The present sequence encodes a GAGE-5 tumour rejection antigen  
 CC precursor (TRAP). The protein is expressed in a number of tumours. In  
 CC contrast the only normal tissue which expresses GAGE TRAP protein is  
 CC testis. Several GAGE TRAPs have been identified (see AAV18717-21). The  
 CC major difference between these proteins and GAGE-1 (AAV05540) is the  
 CC absence of a stretch of 143 bases located at position 379 to 521 of the  
 CC GAGE-1 TRAP sequence. The rest of the sequences show mismatches at  
 CC various positions, with the exception of GAGE-3 whose 5' end is totally  
 CC different from the other GAGE cDNAs for the first 112 bases. This region  
 CC of GAGE-3 cDNA contains a long repeat and a hairpin structure. The  
 CC antigens can be used to diagnose melanomas, characterised by expression  
 CC of a TRAP or presentation of a tumour rejection antigen. Antigens shed  
 CC into blood or urine can be observed and then used to confirm a diagnosis  
 CC of melanoma using cytolytic T cell clone proliferation methodologies.  
 CC Other uses for the processed peptides, include HLA-typing assays for,  
 CC e.g. skin graft or organ transplants  
 XX  
 SQ Sequence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 U; 0 Other;

	PT	Conditions, e.g. cancer.
XX	PS	Example 13; Fig 4; 62pp; English.
XX	CC	The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present invention
XX	SQ	Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;
		Query Match 95.0%; Score 512.8; DB 2; Length 538; Best Local Similarity 98.1%; Pred No. 1.1e-136; Matches 530; Conservative 0; Mismatches 7; Indels 3; Gaps 1;
QY	Db	1 CGGCAGGAGCTGTGAGGCGAGTGTGTGTGTTCCTGCCGTCGGACTCTTTTTCCTCA 60 2 CGGCAGGAGCTGTGAGGCGAGTGTGTGTGTTCCTGCCGTCGGACTCTTTTTCCTCA 61
QY	Db	61 CTGAGATTCATCTGTGTGAATAATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG 120 62 CTGAGATTCATCTGTGTGAATAATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG 118
QY	Db	121 ACCAAGCGCTATGTATACAGCTCTCTGAAATGATTGGGCTATGGCCCCGAGCAGTTCAG 180 119 ACCAAGCGCTATGTATACAGCTCTCTGAAATGATTGGGCTATGGCCCCGAGCAGTTCAG 178
QY	Db	181 TGATGAAGTGGAACCGAACACCTGAAGAAGGGGAACAGCAACTCAACGTGAGATCC 240 179 TGATGAAGTGGAACCGAACACCTGAAGAAGGGGAACAGCAACTCAACGTGAGATCC 238
QY	Db	241 TGCAGCTGTCTCAGAGGGGAGAGGATGAGGAGGATCTGCAAGTCAAGGGCCGAGCCTGA 300 239 TGCAGCTGTCTCAGAGGGGAGAGGATGAGGAGGATCTGCAAGTCAAGGGCCGAGCCTGA 298
QY	Db	301 AGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGTGGTCTCTGA 360 299 AGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGTGGTCTCTGA 358
QY	Db	361 TGGGCGAGGAGATGGACCCGCCAAAATCCAGAGGAGGTGAAAAAGCCCTGAAGAGAGTGA 420 359 TGGGCGAGGAGATGGACCCGCCAAAATCCAGAGGAGGTGAAAAAGCCCTGAAGAGAGTGA 418
QY	Db	421 GCAATCACAGTGTAAAAAGAGCGACGTTGAATGATGACAGGCTGTCTTATGTTGAAA 480 419 GCATCACAGTGTAAAAAGAGCGACGTTGAATGATGACAGGCTGTCTTATGTTGAAA 478
QY	Db	481 TTGTGTTCAATAAATTTCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAAAGAAAAA 540 479 TTGTGTTCAATAAATTTCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAAAGAAAAA 538
		RESULT 10 ADA15802 ID ADA15802 standard; cDNA; 526 BP. XX AC ADA15802; XX DT 06-NOV-2003 (first entry) XX DE Human GAGE-7B cDNA. XX KW Human; GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL; KW human leukocyte antigen; HLA; tumour rejection antigen precursor; KW major histocompatibility complex; MHC; cytolytic T cell proliferation; XX chromosome Xp11.2-p11.4. OS Homo sapiens. XX

```

FH Key Location/Qualifiers
FT CDS 55..408
FT /*tag= a
FT /product= "Human GAGE-7B"
FT /transl_except= (pos:115..162, aa: GPMRPEQSGDEVPEMI)
FT /transl_except= (pos:265..306, aa: HPQTGRPEAHSQEQ)
XX
PN US6509172-B1.
XX
XX 21-JAN-2003.
XX
XX 30-SEP-1998; 98US-00163748.
XX
XX 30-SEP-1998; 98US-00163748.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX De Backer O, Van Den Eynde B, Boon-Falleur T;
XX
XX WPI; 2003-401119/38.
XX P-PSDB; ADA15777.
XX
XX New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor
XX rejection antigen precursors, which complex to major histocompatibility
XX complex molecules to facilitate the proliferation of cytolytic T cells.
XX
XX Claim 1; Col 9-10; 15pp; English.
XX
XX The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the
XX nucleic acid molecules encoding them. The invention also relates to an
XX expression vector comprising an isolated nucleic acid molecule of the
XX invention operably linked to a promoter, a recombinant cell comprising
XX the isolated nucleic acid molecule or the expression vector and an
XX expression kit useful in generating cytolytic T lymphocytes (CTLs) or
XX determining if CTLs are present in a sample comprising the isolated
XX nucleic acid molecule and the isolated nucleic acid that encodes a human
XX leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid
XX molecules encode tumour rejection antigen precursors, which complex to
XX major histocompatibility complex (MHC) molecules to facilitate the
XX proliferation of cytolytic T cells. This sequence represents cDNA
XX encoding the human GAGE-7B polypeptide of the invention. The gene resides
XX on chromosome Xp11.2-p11.4.
XX
XX Sequence 526 BP; 168 A; 109 C; 143 G; 106 T; 0 U; 0 Other;
XX
XX Query Match 94.2%; Score 508.8; DB 7; Length 526;
XX Best Local Similarity 99.6%; Pred. NO. 1.5e-135;
XX Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 29 TGGTTCCTCGCGTCCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTAATATGAGT 88
DB 1 TGGTTCCTCGCGTCCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTAATATGAGT 60
QY 89 TGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGCGCTATGTACGCTCTCTGAA 148
DB 61 TGGCGAGGAGATGACCTATTATTGGCTAGACCAAGCGCTATGTACGCTCTCTGAA 120
QY 149 ATGATTGGCCCTATCGGCGCCGAGCAGTTCAGTGTAGTGAAGTGAACACACACCTGAA 208
DB 121 ATGATTGGCCCTATCGGCGCCGAGCAGTTCAGTGTAGTGAAGTGAACACACACCTGAA 180
QY 209 GAAGGGGAACGAGCACTCAAGCTCAGGATCTGTCAGCTGCTCAGGAGGAGGATGAG 268
DB 181 GAAGGGGAACGAGCACTCAAGCTCAGGATCTGTCAGCTGCTCAGGAGGAGGATGAG 240
QY 269 GGAGCATCTGCAGGTCAAGCGCGGAGCGCTGAAGCTGTAGCCAGAAACAGGTCACCCA 328
DB 241 GGAGCATCTGCAGGTCAAGCGCGGAGCGCTGAAGCTGTAGCCAGAAACAGGTCACCCA 300
QY 329 CAGACTGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 388
DB 301 CAGACTGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 360
QY 389 GAGGAGGTGAAAACCGCTGAAAGAGCAATCACAGTGTAAAAAGAGGACACT 448
DB 361 GAGGAGGTGAAAACCGCTGAAAGAGCAATCACAGTGTAAAAAGAGGACACT 420
QY 449 TCAATATGATGAGGCTGCTCTATGTTGAAATTTGTTCAATAAATCTCCCAATAAAG 508
DB 421 TCAATATGATGAGGCTGCTCTATGTTGAAATTTGTTCAATAAATCTCCCAATAAAG 480
QY 509 CTTTACAGCCTTCTGCAAAAAAATAAAAAA 540
DB 481 CTTTACAGCCTTCTGCAAAAAAATAAAAAA 512
XX
XX RESULT 11
XX ABZ20463
XX ID ABZ20463 standard; cDNA; 530 BP.
XX AC ABZ20463;
XX XX
XX 23-JAN-2003 (first entry)
XX
XX GAGE-2 full length cDNA sequence SEQ ID NO:2890.
XX
XX Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
XX immune response; virology; immunology; microbiology; molecular biology;
XX recombinant DNA technology; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200278516-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US010421.
XX
XX 30-MAR-2001; 2001US-0280255P.
XX 28-AUG-2001; 2001US-0315563P.
XX 09-JAN-2002; 2002US-0347313P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Wang S, Bangur CS, Gaiger A;
XX
XX WPI; 2003-059387/05.
XX P-PSDB; ABP54447.
XX
XX New immunogenic polynucleotides or polypeptides useful for diagnosing,
XX preventing and treating cancer expressing CT or CP mRNA antigens, and in
XX virology, immunology, microbiology, molecular biology and recombinant DNA
XX techniques.
XX
XX Claim 1; SEQ ID NO 2890; 207pp; English.
XX
XX ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
XX ABP54446 to ABP54472 represent protein (II) sequences, from the present
XX invention. (I) and (II) have cytostatic activity and can be used in gene
XX therapy and vaccines. (I), (II), antibodies and compositions from the
XX present invention are useful for diagnosing, preventing and treating
XX cancer, which expresses CT or CP mRNA antigens. They are useful for
XX stimulating immune response. They can also be useful in virology,
XX immunology, microbiology, molecular biology and recombinant DNA
XX techniques. N.B. The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 530 BP; 152 A; 116 C; 155 G; 107 T; 0 U; 0 Other;
XX
XX Query Match 93.5%; Score 504.8; DB 7; Length 530;
XX Best Local Similarity 98.1%; Pred. No. 2.1e-134;
XX Matches 522; Conservative 0; Mismatches 7; Indels 3; Gaps 1;
XX
QY 1 CCCCCAGGAGCTGTGAGGCGAGTGTGTGTGTCTCTGCGCTCCGACTCTTTTCTCTA 60
DB 1 CCCCCAGGAGCTGTGAGGCGAGTGTGTGTGTCTCTGCGCTCCGACTCTTTTCTCTA 60

```





Claim 1; Page 120; 527pp; English.

The invention relates to 1046 novel nucleic acids which are used as markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemotherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, particularly those cancers which display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be used to detect transcripts or genomic sequences corresponding to the markers, in the identification of cells or tissues which mis-express the protein. Cancers which may be targeted include carcinoma (e.g. squamous cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and tumours (e.g. glioma). The present sequence is one of the 1046 novel cancer cell markers

Sequence 530 BP; 89 A; 100 C; 106 G; 183 T; 0 U; 52 Other;

Query Match	56.7%;	Score	306.2;	DB	4;	Length	530;
Best Local Similarity	88.7%;	Pred.	No. 1.9e-77;				
Matches	323;	Conservative	0;	Mismatches	39;	Indels	2;
Gaps	1;						

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179 AGTGATGAAGTGAACACG--AACACCTGAAGAGGGGAAACACGCAACTCAACGTCAGG 236
      |||||
449 AGTNAATGAATGGAGCCACCCNACNCCCTGAANAAGGGNAAACGACACTCAACGTNAGG 390

237 ATCTCTGCAGCTGCTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGCCCGAAGC 296
      |||||
389 ATCTCTGNAGTCNCNAGNAGGAGNAGGATNAGGGNCATNTGCAGTCAAGGCCCGAAGC 330

297 CTGAAGCTGATAGCAGGAAACAGGGTCAACCCACAGACTGGTCTGAGTGTGAAGATGGTC 356
      |||||
329 CTGAAGTCTATGACCCAGGAACAGGGTCNCCCCNACTGGGNGTNAAGTGTNAAAATGGTC 270

357 CTGATGGGCAGAGATGGACCGCCAAATCCAGAGGAGGTGAAACGCCCTGAAGAAGGTG 416
      |||||
269 CTNATGGCAGNANATGGACCCNCAATCCAAAGNAGGTGAAACNCCCTGAANAAGGTG 210

417 AAAAGCAATACACAGTGTATAAAGAAAGGACAGTGTAAATGATGACGGCTGCTCTATGTTG 476
      |||||
209 AAAAGCAATCCAGTGTATAAANAAGGNCGTTGAAATGATGACGGCTGCTCTATGTTG 150

477 GAAATTTGTTCAATAAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAAATAAAA 536
      |||||
149 GAAATTTGTTCAATAAATCTCCCAATAAAGCTTTACAGCCTTNTNAAAAAAATAAAA 90
      |||||

537 AAAAA 540
      |||||
89 AAAA 86

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Search completed: August 6, 2004, 17:02:11  
Job time : 342 secs

Search completed: August 6, 2004, 17:02:11  
Job time : 342 secs

	gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
XX	Sequence 430 BP; 101 A; 102 C; 134 G; 85 T; 0 U; 8 Other;
XX	Query Match 66.7%; Score 360.4; DB 3; Length 430;
XX	Best Local Similarity 97.9%; Pred. No. 4.9e-93;
XX	Matches 369; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
XX	
QY	1 CGCGAGGAGCTGTGAGGACGTCGTGTGGTTCCTGCCGTCGGACTCTTTTCCCTCTA 60
DB	55 CGCAGGGAGCTGTGAGGACGTCGTGTGGTTCCTGCCGTCGGACTCTTTTCCCTCTA 114
QY	61 CTGAGATTCAATCTGTGAAAATATGAGTTGGCGAGAGAATCGACTTAATTATGGCCCTAG 120
DB	115 CTGAGATTCAATCTGTGAAAATATGAGTTGGCGAGAGAATCGACTTAATNA-YGGCCTAG 173
QY	121 ACCAAGCGCGTATGTACAGCCTCTCAAATGATTGGGCCTATPGCGCCGAGCATTCAG 180
DB	174 ACCAAGRCGCTATGTACAGCCTCTCAAATGATTGGGCCTATPGCGCCGAGCATTCAG 233
QY	181 TGATGAAGTGAAACCAGCACACTGAAAGAGGGGAACAGCAACTCAACGTCAGGATCC 240
DB	234 TGATGAAGTGAAACCAGCACACTGAAAGAGGGGAACAGCAACTCAAYGTTCAGGATCC 293
QY	241 TGCAGCTGCTCAGGAGGAGGAGGATCAGGAGCATCTGCAGGTCAAGGCGCGAAGCCTGA 300
DB	294 TGCAGCTGCTCAGGAGGAGGAGGATCAGGAGCATCTGCAGGTCAAGGCGCGAAGCCTGA 353
QY	301 AGCTCATAGCCAGGAAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCCTGA 360
DB	354 AGCTCATAGCCAGGAAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCCTGA 413
QY	361 TGGCGAGGAGATGGACC 377
DB	414 TGGCGAGGAGATGGAMC 430
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ID	AAS60104 standard; cDNA; 530 BP.
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XX	AAS60104;
XX	
DT	29-JAN-2002 (first entry)
XX	
XX	Human cancer agent-sensitive marker #105.
DE	
DE	
KW	Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
KW	squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
KW	lymphocytic leukaemia; lymphoma; plasmacytoma; reticulum cell sarcoma;
XX	Hodgkin's disease; glioma; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200179556-A2.
PD	
PD	25-OCT-2001.
XX	
PF	13-APR-2001; 2001WO-US012132.
XX	
PR	14-APR-2000; 2000US-019753BP.
XX	
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX	
PI	Lillie J, Brown JL, Bolt A, Van Huffel C;
XX	
DR	WPI; 2001-602933/68.
XX	
PT	Novel nucleic acid, used as a marker to determine the effectiveness of
PT	using TAXOL to treat cancer cell growth in individuals.
XX	





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OM nucleic - nucleic search, using sw model

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Perfect score: 532

Sequence: 1 AGCTGTGAGGCAGTGTGTG.....CTGCAGAGAAAAA 532

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 3957288

Minimum DB seq length: 0

Maximum DB seq length: 532

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_or.\*  
21: em\_ov.\*  
22: em\_pat.\*  
23: em\_ph.\*  
24: em\_pl.\*  
25: em\_ro.\*  
26: em\_sts.\*  
27: em\_un.\*  
28: em\_vi.\*  
29: em\_vl.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
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33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rnd.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	532	100.0	532	6	AR028491	AR028491 Sequence
2	532	100.0	532	6	BD231800	BD231800 Isolated
3	532	100.0	532	6	I55854	I55854 Sequence 17
4	532	100.0	532	6	BD132470	BD132470 Isolated
5	524	98.5	524	9	HSU19146	U19146 Human GAGE-
6	517.4	97.3	528	6	AX334151	AX334151 Sequence
7	517.4	97.3	528	9	HSU19145	U19145 Human GAGE-
8	515.8	97.0	527	9	HSU19147	U19147 Human GAGE-
9	513.4	96.5	524	9	AF058988	AF058988 Homo sapi
10	508.8	95.6	526	6	AR275666	AR275666 Sequence
11	508.8	95.6	526	9	AF055474	AF055474 Homo sapi
12	504.4	94.8	528	6	AR275665	AR275665 Sequence
13	504.4	94.8	528	9	AF055473	AF055473 Homo sapi
14	496.8	93.4	530	9	HSU19143	U19143 Human GAGE-
15	350.8	65.9	430	6	AX886264	AX886264 Sequence
16	350.8	65.9	430	6	BD025874	BD025874 Sequence
17	304.6	57.3	530	6	AX284300	AX284300 Sequence
18	302.4	56.8	365	6	AX284692	AX284692 Sequence
19	174.2	32.7	493	9	HSR318881	AJ318881 Homo sapi
20	171.6	32.3	494	6	AX921771	AX921771 Sequence
21	150.6	28.3	441	12	BT007722	BT007722 Synthetic
22	147.4	27.7	506	6	AR415772	AR415772 Sequence
23	147.4	27.7	506	6	BD111325	BD111325 EST and e
24	136	25.6	494	6	AR416094	AR416094 Sequence
25	136	25.6	494	6	BD111647	BD111647 EST and e
26	133.2	25.0	475	6	AX226497	AX226497 Sequence
27	131.8	24.8	500	9	BC054022	BC054022 Homo sapi
28	128	24.1	524	6	AR416095	AR416095 Sequence
29	128	24.1	524	6	BD111848	BD111848 EST and e
30	118	22.2	448	6	AX226538	AX226538 Sequence
31	111.6	21.0	448	6	AX226537	AX226537 Sequence
32	111.4	20.9	529	9	BC009538	BC009538 Homo sapi
33	108	20.3	399	6	AR272357	AR272357 Sequence
34	108	20.3	399	6	AR275938	AR275938 Sequence
35	108	20.3	399	6	AR406213	AR406213 Sequence
36	108	20.3	399	6	AX062442	AX062442 Sequence
37	108	20.3	399	6	AX367359	AX367359 Sequence
38	104.4	19.6	463	9	HSR290447	AJ290447 Homo sapi
39	103.4	19.4	463	6	AX370580	AX370580 Sequence
40	102	19.2	467	9	BC010897	BC010897 Homo sapi
41	101.6	19.1	515	6	BD242364	BD242364 Compounds
42	101.6	19.1	515	6	AR261040	AR261040 Sequence
43	101.6	19.1	515	6	AR278571	AR278571 Sequence
44	101.6	19.1	515	6	AR367267	AR367267 Sequence
45	101.6	19.1	515	6	AR371163	AR371163 Sequence

# ALIGNMENTS

RESULT 1  
AR028491  
LOCUS AR028491 Sequence 17 from patent US 5858689.  
DEFINITION Sequence 17 from patent US 5858689.  
ACCESSION AR028491  
VERSION AR028491.1 GI:5940464  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 532)  
AUTHORS van der Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Palleur,T.  
TITLE Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof

532 bp DNA linear PAT 29-SEP-1999

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JOURNAL Patent: US 5858689-A 17 12-JAN-1999;
FEATURES Location/Qualifiers
source
1..532
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 532; DB 6; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.5e-127; Indels 0; Gaps 0;
Matches 532; Conservative 0; Mismatches 0;

QY 1 AGCTGTGAGCAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60
DB 1 AGCTGTGAGCAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60
QY 61 CATCTGTGTAATATAGTGTGGCAGGAAGATCGACCTATTATGGCCCTAGACCAAGGC 120
DB 61 CATCTGTGTAATATAGTGTGGCAGGAAGATCGACCTATTATGGCCCTAGACCAAGGC 120
QY 121 GCTATGTACAGCTCTCGTAAGTATTGGGCTATGGCCCTAGACCAAGGC 180
DB 121 GCTATGTACAGCTCTCGTAAGTATTGGGCTATGGCCCTAGACCAAGGC 180
QY 181 TGGAAACAGCAACACTGAGAGAGGGGAAACAGCAACTCAACGTCAGGATCTTCAGCTG 240
DB 181 TGGAAACAGCAACACTGAGAGAGGGGAAACAGCAACTCAACGTCAGGATCTTCAGCTG 240
QY 241 CTCAGGAGGAGAGATGAGGAGCATCTGCGAGTCAAGGCCCGAAGCCTGGAAGCTGATA 300
DB 241 CTCAGGAGGAGAGATGAGGAGCATCTGCGAGTCAAGGCCCGAAGCCTGGAAGCTGATA 300
QY 301 GCCAGGAGAGGATGAGGAGCATCTGCGAGTCAAGGCCCGAAGCCTGGAAGCTGATA 360
DB 301 GCCAGGAGAGGATGAGGAGCATCTGCGAGTCAAGGCCCGAAGCCTGGAAGCTGATA 360
QY 361 AGATGGACCCGCCAAATCCAGAGAGGTGAAACCCCTGGAAGAGGTGAAAGCAATCAC 420
DB 361 AGATGGACCCGCCAAATCCAGAGAGGTGAAACCCCTGGAAGAGGTGAAAGCAATCAC 420
QY 421 AGTGTAAAGAGAGCAGTGAATGATGACAGCTCTCTCTATGTTGGAATTTGTTCA 480
DB 421 AGTGTAAAGAGAGCAGTGAATGATGACAGCTCTCTCTATGTTGGAATTTGTTCA 480
QY 481 TTAATAATCTCCCAATAAGCTTTACAGCCTTTCTGCAAGAAAAA 532
DB 481 TTAATAATCTCCCAATAAGCTTTACAGCCTTTCTGCAAGAAAAA 532

RESULT 2
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LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
DEFINITION as molecules encoding the same, and utilization thereof.
ACCESSION BD231800
VERSION BD231800.1 GI:33041570
KEYWORDS JP 2002509859-A/10.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Bruggen,P.V.D., Eynde,B.V.D., Debacker,O. and Falleur,T.B.
Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
as molecules encoding the same, and utilization thereof
Patent: JP 2002509859-A 10 02-APR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
OS Homo sapiens (human)
PN JP 2002509859-A/10
PD 02-APR-2002
PF 12-JAN-1999 JP 2000528586
PR 23-JAN-1998 US 09/012818
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,
THIERRY BOON FALLEUR
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PC C07K4/12,C12N15/09,C12P21/00,C12Q1/00,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
STRANDEDNESS:single,TOPOLOGY:linear
FH Key Location/Qualifiers
FT source 1..532
/organism="Homo sapiens (human)".

FEATURES Location/Qualifiers
source
1..532
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 532; DB 6; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.5e-127; Indels 0; Gaps 0;
Matches 532; Conservative 0; Mismatches 0;

QY 1 AGCTGTGAGCAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60
DB 1 AGCTGTGAGCAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60
QY 61 CATCTGTGTAATATAGTGTGGCAGGAAGATCGACCTATTATGGCCCTAGACCAAGGC 120
DB 61 CATCTGTGTAATATAGTGTGGCAGGAAGATCGACCTATTATGGCCCTAGACCAAGGC 120
QY 121 GCTATGTACAGCTCTCGTAAGTATTGGGCTATGGCCCTAGACCAAGGC 180
DB 121 GCTATGTACAGCTCTCGTAAGTATTGGGCTATGGCCCTAGACCAAGGC 180
QY 181 TGGAAACAGCAACACTGAGAGAGGGGAAACAGCAACTCAACGTCAGGATCTTCAGCTG 240
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QY 301 GCCAGGAGAGGATGAGGAGCATCTGCGAGTCAAGGCCCGAAGCCTGGAAGCTGATA 360
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QY 361 AGATGGACCCGCCAAATCCAGAGAGGTGAAACCCCTGGAAGAGGTGAAAGCAATCAC 420
DB 361 AGATGGACCCGCCAAATCCAGAGAGGTGAAACCCCTGGAAGAGGTGAAAGCAATCAC 420
QY 421 AGTGTAAAGAGAGCAGTGAATGATGACAGCTCTCTCTATGTTGGAATTTGTTCA 480
DB 421 AGTGTAAAGAGAGCAGTGAATGATGACAGCTCTCTCTATGTTGGAATTTGTTCA 480
QY 481 TTAATAATCTCCCAATAAGCTTTACAGCCTTTCTGCAAGAAAAA 532
DB 481 TTAATAATCTCCCAATAAGCTTTACAGCCTTTCTGCAAGAAAAA 532

RESULT 3
BD231800 532 bp DNA linear PAT 07-OCT-1997
LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
DEFINITION Sequence 17 from patent US 5648226.
ACCESSION I55854
VERSION I55854
KEYWORDS I55854.1 GI:2476648
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 532)
AUTHORS Van den Eynde,B., DeBacker,O. and Boon-Falleur,T.
TITLE Isolated peptides derived from tumor rejection antigens, and their use
JOURNAL Patent: US 5648226-A 17 15-JUL-1997;
FEATURES Location/Qualifiers
source
1..532
/organism="unknown"
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ORIGIN		/mol_type="unassigned DNA"	
Query Match		100.0%; Score 532; DB 6; Length 532;	
Best Local Similarity		100.0%; Pred. No. 1.5e-127;	
Matches 532; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	AGCTGTGAGGCAAGTGTCTGTGGTTCCTGCGGTCGGACTCTTTTCCTCTACTGAGATT	60
Db	1	AGCTGTGAGGCAAGTGTCTGTGGTTCCTGCGGTCGGACTCTTTTCCTCTACTGAGATT	60
QY	61	CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC	120
Db	61	CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC	120
QY	121	GCTATGTACAGGCTCTCTGAAGTGATTGGGCTATGCGGCCCGAGCAGTTTCAGTGAATGAAG	180
Db	121	GCTATGTACAGGCTCTCTGAAGTGATTGGGCTATGCGGCCCGAGCAGTTTCAGTGAATGAAG	180
QY	181	TGGAACCAACACCTGAGAGGGGAACCACTCAAGTCAAGGATCCTGCGAGCTG	240
Db	181	TGGAACCAACACCTGAGAGGGGAACCACTCAAGTCAAGGATCCTGCGAGCTG	240
QY	241	CTCAGAGGAGGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATA	300
Db	241	CTCAGAGGAGGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATA	300
QY	301	GCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTGATGGGCAGG	360
Db	301	GCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTGATGGGCAGG	360
QY	361	AGATGGACCCGCCCAATCCAGAGGAGTGAACCGCTGAGAGAGTGAAGAGCAATCAC	420
Db	361	AGATGGACCCGCCCAATCCAGAGGAGTGAACCGCTGAGAGAGTGAAGAGCAATCAC	420
QY	421	AGTGTATAAAGAGGACGTTGAAATGATGAGGCTGCTCCTATGTTGAAAATTTGTTCA	480
Db	421	AGTGTATAAAGAGGACGTTGAAATGATGAGGCTGCTCCTATGTTGAAAATTTGTTCA	480
QY	481	TTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA	532
Db	481	TTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA	532
RESULT 4		BD132470	
LOCUS		532 bp DNA linear PAT 18-SEP-2002	
DEFINITION		Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof.	
ACCESSION		BD132470	
VERSION		BD132470.1 GI:23227415	
KEYWORDS		JP 2002507112-A/10.	
SOURCE		synthetic construct	
ORGANISM		artificial sequences.	
REFERENCE		1 (bases 1 to 532)	
AUTHORS		Debacker, O., Eynde, B.V.D. and Falleur, T.B.	
TITLE		Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof	
JOURNAL		Patent: JP 2002507112-A 10 05-MAR-2002;	
COMMENT		LUDWIG INSTITUTE FOR CANCER RESEARCH	
		PN JP 2002507112-A/10	
		PD 05-MAR-2002	
		PF 23-JUN-1997 JP 1998503430	
		PR 24-JUN-1996 US 08/669161	
		PI OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON FALLEUR PC	
		A61K38/00, A61K45/05, C07K7/00, C07K14/82, C12N15/00 CC	
		Strandedness: Single;	
		CC Topology: Linear;	
FH Key		Location/Qualifiers.	
source		1..532	
		/organism="synthetic construct"	

ORIGIN		/mol_type="genomic DNA"	
Query Match		100.0%; Score 532; DB 6; Length 532;	
Best Local Similarity		100.0%; Pred. No. 1.5e-127;	
Matches 532; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	AGCTGTGAGGCAAGTGTCTGTGGTTCCTGCGGTCGGACTCTTTTCCTCTACTGAGATT	60
Db	1	AGCTGTGAGGCAAGTGTCTGTGGTTCCTGCGGTCGGACTCTTTTCCTCTACTGAGATT	60
QY	61	CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC	120
Db	61	CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGC	120
QY	121	GCTATGTACAGGCTCTCTGAAGTGATTGGGCTATGCGGCCCGAGCAGTTTCAGTGAATGAAG	180
Db	121	GCTATGTACAGGCTCTCTGAAGTGATTGGGCTATGCGGCCCGAGCAGTTTCAGTGAATGAAG	180
QY	181	TGGAACCAACACCTGAGAGGGGAACCACTCAAGTCAAGGATCCTGCGAGCTG	240
Db	181	TGGAACCAACACCTGAGAGGGGAACCACTCAAGTCAAGGATCCTGCGAGCTG	240
QY	241	CTCAGAGGAGGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATA	300
Db	241	CTCAGAGGAGGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATA	300
QY	301	GCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTGATGGGCAGG	360
Db	301	GCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTGATGGGCAGG	360
QY	361	AGATGGACCCGCCCAATCCAGAGGAGTGAACCGCTGAGAGAGTGAAGAGCAATCAC	420
Db	361	AGATGGACCCGCCCAATCCAGAGGAGTGAACCGCTGAGAGAGTGAAGAGCAATCAC	420
QY	421	AGTGTATAAAGAGGACGTTGAAATGATGAGGCTGCTCCTATGTTGAAAATTTGTTCA	480
Db	421	AGTGTATAAAGAGGACGTTGAAATGATGAGGCTGCTCCTATGTTGAAAATTTGTTCA	480
QY	481	TTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA	532
Db	481	TTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA	532
RESULT 5		HSU19146	
LOCUS		Human GAGE-5 protein mRNA, complete cds.	
DEFINITION		524 bp mRNA linear PRI 04-DEC-1995	
ACCESSION		U19146	
VERSION		U19146.1 GI:914906	
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1 (bases 1 to 524)	
AUTHORS		Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S. and Boon, T.	
TITLE		A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma	
JOURNAL		J. Exp. Med. 182 (3), 689-698 (1995)	
MEDLINE		95378788	
PUBMED		7544395	
REFERENCE		2 (bases 1 to 524)	
AUTHORS		Van Den Eynde, B.J.	
TITLE		Direct Submission	
JOURNAL		Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium	
FEATURES		Location/Qualifiers	
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## CDS

## ORIGIN

Query Match 98.5%; Score 524; DB 9; Length 524;  
Best Local Similarity 100.0%; Pred. No. 1.8e-125;  
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGTGAGGAGTCTGTGTGTTCTTCCGCTCCGACTCTTTTCTCTACTCAGATT 60  
Db 1 AGCTGTGAGGAGTCTGTGTGTTCTTCCGCTCCGACTCTTTTCTCTACTCAGATT 60  
QY 61 CATCTGTGAAATATGATGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 120  
Db 61 CATCTGTGAAATATGATGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 120  
QY 121 GCTATGTACAGCTCTCTGAAGTATTGGGCTTATGCGGCCGAGCAGTTCAGTGATGAAG 180  
Db 121 GCTATGTACAGCTCTCTGAAGTATTGGGCTTATGCGGCCGAGCAGTTCAGTGATGAAG 180  
QY 181 TGGAAACAGCAACACCTGAAGGAGGAAACAGCAACTCAACGTCAGGATCTGCGAGCTG 240  
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QY 241 CTCAGGAGGAGAGATGAGGAGCATCTGCAAGTCAAGGCGGAAAGCTGAAGCTGATA 300  
Db 241 CTCAGGAGGAGAGATGAGGAGCATCTGCAAGTCAAGGCGGAAAGCTGAAGCTGATA 300  
QY 301 GCCAGGAACAGGTCACCCACAGACTGGTGTGAGTGTGAAGATGGTCTGATGGGCGAG 360  
Db 301 GCCAGGAACAGGTCACCCACAGACTGGTGTGAGTGTGAAGATGGTCTGATGGGCGAG 360  
QY 361 AGATGGACCCGCAAAATCCAGAGGAGGTGAAAGCCCTGGAAGAGGTGAAAGCAATCAC 420  
Db 361 AGATGGACCCGCAAAATCCAGAGGAGGTGAAAGCCCTGGAAGAGGTGAAAGCAATCAC 420  
QY 421 AGTGTAAAGAGGACAGTTGAATGATGACAGGCTGCTCTATGTTGGAAATTTGTTCA 480  
Db 421 AGTGTAAAGAGGACAGTTGAATGATGACAGGCTGCTCTATGTTGGAAATTTGTTCA 480  
QY 481 TTAAATTTCTCCATAAGCTTTACAGCTTTTACAGCTTTCTGCAAGAAA 524  
Db 481 TTAAATTTCTCCATAAGCTTTACAGCTTTTACAGCTTTCTGCAAGAAA 524

## RESULT 6

AX334151  
LOCUS AX334151 528 bp DNA linear PAT 09-JAN-2002  
DEFINITION Sequence 4660 from Patent WO0194629.  
ACCESSION AX334151  
VERSION AX334151.1 GI:18124870  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

## REFERENCE

1  
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ehner,R., Endress,G.,  
Horrigan,S., Soppet,D.R. and Weaver,Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets  
JOURNAL Patent: WO 0194629-A 4660 13-DEC-2001;

FEATURES  
source

Avalon Pharmaceuticals (US)  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 97.3%; Score 517.4; DB 6; Length 528;  
Best Local Similarity 99.8%; Pred. No. 9.2e-124;  
Matches 518; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGCTGTGAGGAGTCTGTGTGTTCTTCCGCTCCGACTCTTTTCTCTACTCAGATT 60  
Db 9 AGCTGTGAGGAGTCTGTGTGTTCTTCCGCTCCGACTCTTTTCTCTACTCAGATT 68  
QY 61 CATCTGTGAAATATGATGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 120  
Db 69 CATCTGTGAAATATGATGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 128  
QY 121 GCTATGTACAGCTCTCTGAAGTATTGGGCTTATGCGGCCGAGCAGTTCAGTGATGAAG 180  
Db 129 GCTATGTACAGCTCTCTGAAGTATTGGGCTTATGCGGCCGAGCAGTTCAGTGATGAAG 188  
QY 181 TGGAAACAGCAACACCTGAAGGAGGAAACAGCAACTCAACGTCAGGATCTGCGAGCTG 240  
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QY 241 CTCAGGAGGAGAGATGAGGAGCATCTGCAAGTCAAGGCGGAAAGCTGAAGCTGATA 300  
Db 249 CTCAGGAGGAGAGATGAGGAGCATCTGCAAGTCAAGGCGGAAAGCTGAAGCTGATA 308  
QY 301 GCCAGGAACAGGTCACCCACAGACTGGTGTGAGTGTGAAGATGGTCTGATGGGCGAG 360  
Db 309 GCCAGGAACAGGTCACCCACAGACTGGTGTGAGTGTGAAGATGGTCTGATGGGCGAG 368  
QY 361 AGATGGACCCGCAAAATCCAGAGGAGGTGAAAGCCCTGGAAGAGGTGAAAGCAATCAC 420  
Db 369 AGATGGACCCGCAAAATCCAGAGGAGGTGAAAGCCCTGGAAGAGGTGAAAGCAATCAC 428  
QY 421 AGTGTAAAGAGGACAGTTGAATGATGACAGGCTGCTCTATGTTGGAAATTTGTTCA 480  
Db 429 AGTGTAAAGAGGACAGTTGAATGATGACAGGCTGCTCTATGTTGGAAATTTGTTCA 488  
QY 481 TTAAATTTCTCCATAAGCTTTACAGCTTTTACAGCTTTCTGCAAA 519  
Db 489 TTAAATTTCTCCATAAGCTTTACAGCTTTTACAGCTTTCTGCAAA 527

## RESULT 7

HSU19145  
LOCUS Human GAGE-4 protein mRNA, complete cds.  
DEFINITION U19145  
ACCESSION U19145  
VERSION U19145.1 GI:914904  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

## REFERENCE

AUTHORS Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S.  
and Boon,T.  
TITLE A new family of genes coding for an antigen recognized by  
autologous cytolytic T lymphocytes on a human melanoma  
J. Exp. Med. 182 (3), 689-698 (1995)  
JOURNAL MEDLINE  
PUBMED 754395  
REFERENCE 2 (bases 1 to 528)  
AUTHORS Van den Eynde,B.J.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute  
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium



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LOCUS AF058988 524 bp mRNA linear PRI 11-JUL-1998
DEFINITION Homo sapiens melanoma antigen related GAGE-7 mRNA, complete cds.
ACCESSION AF058988
VERSION AF058988.1 GI:3300089
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 524)
AUTHORS Chen, M.E., Lin, S.-H., Chung, L.W.K. and Sikes, R.A.
TITLE Isolation and characterization of PAGE-1 and GAGE-7: new genes
JOURNAL expressed in the LNCAP prostate cancer progression model that share
REFERENCE homology with melanoma associated antigens
AUTHORS J. Biol. Chem. (1998) In press
TITLE 2 (bases 1 to 524)
AUTHORS Chen, M.E., Lin, S.-H., Chung, L.W.K. and Sikes, R.A.
JOURNAL Direct Submission
SUBMITTED (07-APR-1998) Urology, University of Virginia, Box 422,
CHARLOTTESVILLE, VA 22908, USA
FEATURES
LOCATION/Qualifiers
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/db_xref="taxon:9606"
/cell_line="LNCap; C4-2"
/note="isolated from prostate cancer cell lines by
differential display PCR; expression pattern correlates
with progression from androgen sensitive to androgen
insensitive in the human prostate cancer progression model
LNCap to C4-2"
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ORIGIN
Query Match 96.5%; Score 513.4; DB 9; Length 524;
Best Local Similarity 99.0%; Pred. No. 1e-122;
Matches 514; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 AGCTCTGAGGAGTCTGTGTGTTCTTCCTCGCGTCCGGACTCTTTTCTCTCTACTCAGATT 60
DB 6 AGCTGTGAGGAGTCTGTGTGTTCTTCCTCGCGTCCGGACTCTTTTCTCTCTACTCAGATT 65
QY 61 CATCTGTGTGAATATGATTGGCGAGGAAGATCGACCTATTATTGGCTTAGACCAAGGC 120
DB 66 CATCTGTGTGAATATGATTGGCGAGGAAGATCGACCTATTATTGGCTTAGACCAAGGC 125
QY 121 GCTATGTACAGCCTCTCAAGTATTGGCCCTATCGGCCCGCAGGAGTTCAGTATGAAG 180
DB 126 GCTATGTACAGCCTCTCAAGTATTGGCCCTATCGGCCCGCAGGAGTTCAGTATGAAG 185
QY 181 TGGAAACAGCAACCTCTGAAGAAGGGGAACAGCAACTCAACGTCAGGATCCTCAGCTG 240
DB 186 TGGAAACAGCAACCTCTGAAGAAGGGGAACAGCAACTCAACGTCAGGATCCTCAGCTG 245
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QY 301 GCCAGGAACAGGGTCACCCACAGACTGGTGTGAGTGTGAAGTGGTCTTGTATGGCAGG 360
DB 306 GCCAGGAACAGGGTCACCCACAGACTGGTGTGAGTGTGAAGTGGTCTTGTATGGCAGG 365
QY 361 AGATGGACCCGCCAAATCCAGAGGAGTGAAGACCCCTGAAAGAGGTGAAGAGCAATCAC 420
DB 366 AGATGGACCCGCCAAATCCAGAGGAGTGAAGACCCCTGAAAGAGGTGAAGAGCAATCAC 425
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QY 421 AGTGTATAAAGAGCAGCTTGAAATGATGAGGCTGCTCTCTATGTTGAAATTTGTTCA 480
DB 426 AGTGTATAAAGAGCAGCTTGAAATGATGAGGCTGCTCTCTATGTTGAAATTTGTTCA 485
QY 481 TTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAA 519
DB 486 TTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAA 524
RESULT 10
LOCUS AR275666 526 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 2 from patent US 6509172.
ACCESSION AR275666
VERSION AR275666.1 GI:29709168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 526)
AUTHORS De Backer, O., Van den Eynde, B. and Boon-Falleur, T.
TITLE Isolated, truncated nucleic acid which are members of the gage, and
uses thereof
JOURNAL Patent: US 6509172-A 2 21-JAN-2003;
FEATURES Location/Qualifiers
source 1..526
/organism="unknown"
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Query Match 95.6%; Score 508.8; DB 6; Length 526;
Best Local Similarity 99.6%; Pred. No. 1.6e-121;
Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 21 TGGTTCTGCGCTCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTGAATATGAGT 80
DB 1 TGGTTCTGCGCTCGGACTCTTTTCTCTACTGAGATTTCATCTGTGTGAATATGAGT 60
QY 81 TGGCGAGGAAGATCGACCTATTATGGCTAGACCAAGCGCTATGTACAGCTCTCTGAA 140
DB 61 TGGCGAGGAAGATCGACCTATTATGGCTAGACCAAGCGCTATGTACAGCTCTCTGAA 120
QY 141 GTGATTGGGCCCTATGCGGCCGAGCAGTTTCAGTGATGAAGTGAACCAACACCTGAA 200
DB 121 ATGATTGGGCCCTATGCGGCCGAGCAGTTTCAGTGATGAAGTGAACCAACACCTGAA 180
QY 201 GAAGGGGAACAGCAACTCAACGTCAGSATCCTCAGCTGCTCAGGAGGAGAGGATGAG 260
DB 181 GAAGGGGAACAGCAACTCAACGTCAGSATCCTCAGCTGCTCAGGAGGAGAGGATGAG 240
QY 261 GGAGCATCTGCAAGTCAAGGCCGAGCCTGAAGCTGATAGCAGGAACAGGGTCACCCA 320
DB 241 GGAGCATCTGCAAGTCAAGGCCGAGCCTGAAGCTGATAGCAGGAACAGGGTCACCCA 300
QY 321 CAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGGAGATGGACCCGCAATCCA 380
DB 301 CAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGGAGATGGACCCGCAATCCA 360
QY 381 GAGGAGTGAAGAGCCTGGAAGAGGTGAAAAGCAATCACAGTGTAAAAAGAGGACGCT 440
DB 361 GAGGAGTGAAGAGCCTGGAAGAGGTGAAAAGCAATCACAGTGTAAAAAGAGGACGCT 420
QY 441 TGAATGATGAGCTGCTCTCTATGTTGGAATTTGTTCAATTAATTTCCCAATTAAG 500
DB 421 TGAATGATGAGCTGCTCTCTATGTTGGAATTTGTTCAATTAATTTCCCAATTAAG 480
QY 501 CTTTACAGCCTTCTGCAAGAAAAA 532
DB 481 CTTTACAGCCTTCTGCAAGAAAAA 512
RESULT 11
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AF055474
LOCUS Homo sapiens GAGE-7B mRNA 526 bp mRNA linear PRI 01-MAY-2000
DEFINITION Homo sapiens GAGE-7B mRNA, complete cds.
ACCESSION AF055474
VERSION AF055474.1 GI:3511024
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 526)
AUTHORS De Backer, O., Arden, K.C., Boretti, M., Vantomme, V., De Smet, C.,
Czekay, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van den
Eynde, B., Boon, T. and van der Bruggen, P.
TITLE Characterization of the GAGE genes that are expressed in various
human cancers and in normal testis
JOURNAL Cancer Res. 59 (13), 3157-3165 (1999)
MEDLINE 99323388
PubMed 10397259
REFERENCE 2 (bases 1 to 526)
AUTHORS De Backer, O.R.Y.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-1998) Ludwig Institute for Cancer Research,
Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium
FEATURES
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Query Match 95.6%; Score 508.8; DB 9; Length 526;
Best Local Similarity 99.6%; Pred. No. 1.6e-121;
Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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22 TGGTCTCTGCGCCGACGCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGT 60
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Db 421 TGAATGATGATGAGGCTGCTCTATGTTGGAAATTTGTTCAATTAATAATCTCCCAATAAG 480
Qy 501 CTTTACAGCCTTCTGCAAGAAAAA 532
Db 481 CTTTACAGCCTTCTGCAAGAAAAA 512

RESULT 12
LOCUS AR275665 528 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6509172.
ACCESSION AR275665
VERSION AR275665.1 GI:29709167
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 528)
AUTHORS De Backer, O., Van den Eynde, B. and Boon-Palleur, T.
TITLE Isolated, truncated nucleic acid which are members of the gage, and
uses thereof
JOURNAL Patent: US 6509172-A 1 21-JAN-2003;
FEATURES Location/Qualifiers
source
1..528
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 94.8%; Score 504.4; DB 6; Length 528;
Best Local Similarity 98.3%; Pred. No. 2.2e-120;
Matches 521; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
Qy 3 CTGTGAGGAGGCTGCTGTGTGTTCTCTGCGCTCGGACTCTTTTCTCTACTGAGTTCA 62
Db 1 CTGTGAGGAGGCTGCTGTGTGTTCTCTGCGCTCGGACTCTTTTCTCTACTGAGTTCA 60
Qy 63 TCTGTGTGAAATATGAGTTGGCGAGGAAGATCCACCTATTATTGGCTAGACCAAGCGC 122
Db 61 TCTGTGTGAAATATGAGTTGGCGAGGAAGATCCACCTATTATTGGCTAGACCAAGCGC 117
Qy 123 TATGTACAGCCTCTCTGAGTGTGTTGGGCTTATGCGGCCGAGCAGTTTCACTGATGAGTG 182
Db 118 TACGTAGAGCCTCTCTGAAATGATTGGGCTTATGCGGCCGAGCAGTTTCACTGATGAGTG 177
Qy 183 GATCCAGCAACACTGAGAGAGGGGACAGCAACTCAAGCTCAGATCTCTGAGCTGCT 242
Db 178 GATCCAGCAACACTGAGAGAGGGGACAGCAACTCAAGCTCAGATCTCTGAGCTGCT 237
Qy 243 CAGGAGGAGGAGGATGAGGAGCATCTGCAAGGTCAAGGGCCGAGCCTGAAGCTGATAGC 302
Db 238 CAGGAGGAGGAGGATGAGGAGCATCTGCAAGGTCAAGGGCCGAGCCTGAAGCTGATAGC 297
Qy 303 CAGGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGAGGAG 362
Db 298 CAGGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGGAGGAG 357
Qy 363 ATGACCCCGCAATCCAGAGAGGTTGAAACCCCTGAGAGAGTGAAGAGCAATCACAG 422
Db 358 ATGACCCCGCAATCCAGAGAGGTTGAAACCCCTGAGAGAGTGAAGAGCAATCACAG 417
Qy 423 TGTTTAAAGAAAGGACGCTTGAATATGATGAGGCTGCTCTATGTTGAAATTTGTTCAAT 482
Db 418 TGTTTAAAGAAAGGACGCTTGAATATGATGAGGCTGCTCTATGTTGAAATTTGTTCAAT 477
Qy 483 AAAATTTCTCCCAATAAGCTTTTACAGCTTTCTCAAAGAAAAA 532
Db 478 AAAATTTCTCCCAATAAGCTTTTACAGCTTTCTCAAAGAAAAA 527

RESULT 13
LOCUS AF055473 528 bp mRNA linear PRI 01-MAY-2000
DEFINITION Homo sapiens GAGE-8 mRNA, complete cds.
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Db 307 GCCAGGACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCCTGATGGGCAGG 366  
QY 361 AGATGACCCGCCAATCCAGAGAGGTGAAACGGCTGAAGAAGGTGAAAAACAATCAC 420  
Db 367 AGATGACCCGCCAATCCAGAGAGGTGAAACGGCTGAAGAAGGTGAAAAACAATCAC 426  
QY 421 AGTGTAAAGAGAGGACGCTTGAATCATGACGGCTGCTCTATGTTGGAAATTTGTCA 480  
Db 427 AGTGTAAAGAGAGACGCTTGAATCATGACGGCTGCTCTATGTTGGAAATTTGTCA 486  
QY 481 TTAATAATTCCTCCATAAAGCTTTACAGCCTTCTGCAAAAGAAA 524  
Db 487 TTAATAATTCCTCCATAAAGCTTTACAGCCTTCTGCAAAAGAAA 530

## RESULT 15

AX886264

## LOCUS

AX886264 Sequence 2127 from Patent EPI033401. 430 bp DNA linear PAT 18-DEC-2003

## DEFINITION

AX886264

## ACCESSION

AX886264.1

## VERSION

GI:40043251

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1

Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.

## AUTHORS

Expressed sequence tags and encoded human proteins

## TITLE

Patent: EP 1033401-A 2127 06-SEP-2000;

## JOURNAL

Genset (FR)

## FEATURES

Location/Qualifiers

1..430

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

202..&gt;429

/note="unnamed protein product; Protein sequence is in

conflict with the conceptual translation"

/codon\_start=1

/protein\_id="CAF00402.1"

/db\_xref="GI:40043252"

/translations="MIGPMRPEOFSDVEVPATPEEGEPATQXODPAAAXGDEDEGASA

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## ORIGIN

Query Match

Best Local Similarity 97.6%; Pred. No. 2e-80;

Matches 360; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 1 AGCTGTGAGGACGTGCTGTGGTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60

Db 63 AGCTGTGAGGACGTGCTGTGGTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 122

QY 61 CATCTGTGCAATATGAGTTGGCGAGAGATCGACTATTATTGGCCTAGACCAAGGC 120

Db 123 CATCTGTGCAATATGAGTTGGCGAGAGATCGACTATTATTGGCCTAGACCAAGGC 181

QY 121 GCTATGTACAGCCTCTGAAAGTATGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAG 180

Db 182 GCTATGTACAGCCTCTGAAAGTATGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAG 241

QY 181 TGGACCAAGCAACACCTGAGAGAGGGGAACAGCAACTCAACGTGAGGATCCTGCGCTG 240

Db 242 TGGACCAAGCAACACCTGAGAGAGGGGAACAGCAACTCAAGTCTGAGGATCCTGCGCTG 301

QY 241 CTGAGGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGGCCGAGCCTGGAAGCTGATA 300

Db 302 CTGAGGAGGAGAGGATGAGGAGCATCTGAGGTCAAGGGCCGAGCCTGGAAGCTGATA 361

QY 301 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGCAGG 360

Db 362 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGCAGG 421

QY 361 AGATGGACC 369  
Db 422 AGATGGAMC 430

Search completed: August 6, 2004, 20:11:59  
Job time : 2252 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 19:16:15 ; Search time 2412 Seconds  
(without alignments)  
6586.517 Million cell updates/sec

Title: US-09-782-745-17  
Perfect score: 532  
Sequence: 1 AGCTGTAGGCGAGTCTGTG.....CTGCCAAGAAAAA 532

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 27952390

Minimum DB seq length: 0  
Maximum DB seq length: 532

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512.8	96.4	527	12	BI826605
2	510.4	95.9	521	13	BX108227
3	506.6	95.2	517	14	CF780547
4	490.2	92.1	509	12	BI868671

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C 5 476.4 89.5 489 9 AA447559
C 6 452.2 85.0 457 10 AW510753
C 7 443.6 83.4 464 9 AA738037
C 8 442.2 83.1 447 9 AI381509
C 9 438.6 82.4 480 12 BG120336
C 10 436 82.0 505 14 CB115693
C 11 431.6 81.1 450 9 AA760996
C 12 417 78.4 455 9 AI187350
C 13 407.4 76.6 418 9 AW016546
C 14 398.8 75.0 426 9 AA868226
C 15 377.8 71.0 383 12 BM836228
C 16 372.8 70.1 419 9 AA448542
C 17 369 69.4 445 11 BC005363
C 18 360.6 67.8 412 9 AW102587
C 19 334.4 62.9 384 9 AA913206
C 20 331 62.2 383 13 EX283580
C 21 318.8 59.9 397 12 BG206349
C 22 314.8 59.2 341 12 BP431265
C 23 314 59.0 398 9 AA918604
C 24 307.2 57.7 333 13 BU533718
C 25 300.8 56.5 320 12 BM836021
C 26 273.6 51.4 457 14 CF780497
C 27 269.8 50.7 275 14 CB147043
C 28 269.8 50.7 275 14 CB150355
C 29 269.8 50.7 275 14 CB157288
C 30 250.4 47.1 256 12 BG181480
C 31 231.8 43.6 258 12 BG186708
C 32 226.6 42.0 261 12 BG184057
C 33 223.4 42.0 245 12 BG199060
C 34 221.6 41.7 245 12 BG212621
C 35 216.6 40.7 292 12 BG212622
C 36 213.2 40.1 245 12 BG208433
C 37 207.6 39.0 507 9 AA972716
C 38 206.4 38.8 224 9 AA738394
C 39 205.4 38.6 256 12 BG216461
C 40 205.2 38.6 524 11 AF318372
C 41 198.8 37.4 520 14 CB961487
C 42 195.4 36.7 197 9 AI968311
C 43 192.8 36.2 226 12 BG220441
C 44 192.4 36.2 499 12 BG354572
C 45 178.6 33.6 503 9 AI742551
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#### ALIGNMENTS

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BI826605
LOCUS BI826605 527 bp mRNA linear EST 04-OCT-2001
DEFINITION 603077056F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5168892 5',
mRNA sequence.
ACCESSION BI826605
VERSION BI826605.1 GI:15938155
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 527)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11419 row: p column: 13
High quality sequence stop: 519.
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FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5168892"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_lib="NIH_MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
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ORIGIN

Query Match 96.4%; Score 512.8; DB 12; Length 527;  
Best Local Similarity 99.4%; Pred. No. 1.7e-104;  
Matches 525; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 CTGTGAGGAGTGTGTGTCTCTGCGTCCGGACTCTTTTCTCTACTGAGATCA 62  
DB 1 CTGTGAGGAGTGTGTGTCTCTGCGTCCGGACTCTTTTCTCTACTGAGATCA 60  
QY 63 TCTGTGTAATATGAGTTGCGAGGAGATCGACCTATTATGGCTTAGACCAAGGCG 122  
DB 61 TCTGTGTAATATGAGTTGCGAGGAGATCGACCTATTATGGCTTAGACCAAGGCG 120  
QY 123 TATGTACAGCTCTCTGAAGTGATTTGGGCTATGGGCGCCGAGCAGTTTCAGTGATGAAGTG 182  
DB 121 TATGTACAGCTCTCTGAATGATTTGGGCTATGGGCGCCGAGCAGTTTCAGTGATGAAGTG 180  
QY 183 GAACACGACACCTCTGAAGAGGGGAACACGACACTCAACTCAGGATCTCTGAGCTGCT 242  
DB 181 GAACACGACACCTCTGAAGAGGGGAACACGACACTCAACTCAGGATCTCTGAGCTGCT 240  
QY 243 CAGGAGGAGAGGATGAGGAGATCTGCAGGTCAAGGGCGGAGCCTGAAGCTGATAGC 302  
DB 241 CAGGAGGAGAGGATGAGGAGATCTGCAGGTCAAGGGCGGAGCCTGAAGCTGATAGC 300  
QY 303 CAGGAAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAGATGCTCTGATGGGACGAG 362  
DB 301 CAGGAAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAGATGCTCTGATGGGACGAG 360  
QY 363 ATGGACCCGCCAATCCAGAGGAGTGAAACCGCTGAGAGGTGAAAAGCAATCAACAG 422  
DB 361 ATGGACCCGCCAATCCAGAGGAGTGAAACCGCTGAGAGGTGAAAAGCAATCAACAG 420  
QY 423 TGTAAAGAGGACGCTTGAATGATGAGGCTGCTCTATGTTGAAATTTGTTCAAT 482  
DB 421 TGTAAAGAGGACGCTTGAATGATGAGGCTGCTCTATGTTGAAATTTGTTCAAT 480  
QY 483 AAAATTTCCCAATAAAGCTTTACAGCTTTCTGCAAGGAAAAA 530  
DB 481 AAAATTTCCCAATAAAGCTTTACAG-CTTCTGCAAGGAAAAA 527

RESULT 2  
BX108227  
LOCUS  
DEFINITION  
BX108227 NCI CGAP GC3 Homo sapiens cdna clone IMAGEp998K213161 ;  
IMAGE:1256204, mRNA sequence.  
ACCESSION  
BX108227  
VERSION  
BX108227.1 GI:27835080  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 521)  
Ebert L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
Radelof, U., Schneider, D. and Korn, B.  
Human Unigeneset - RZPD3  
JOURNAL  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp998K213161.  
RZPDLIB; I.M.A.G.E. cdna clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/cloneCards/cgi-  
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACAGAAACAGCTATGAC.

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGp998K213161 ; IMAGE:1256204"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GC3"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cdna was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cdna was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT7T3  
vector. Library is not normalized. Library was  
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 95.9%; Score 510.4; DB 13; Length 521;  
Best Local Similarity 98.8%; Pred. No. 5.8e-104;  
Matches 514; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 11 CAGTGCTGTGTGTCTCTGCGTCCGACACTCTTTTCTCTACTGAGATTCATCTGTG 70  
DB 1 CAGTGCTGTGTGTGTCTCTGCGTCCGACACTCTTTTCTCTACTGAGATTCATCTGTG 60  
QY 71 AAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTTAGACCAAGGCGCTATGTACA 130  
DB 61 AAATATGAGTTGGCGAGGAAGATCGACCTGTATTGGCTTAGTCCAAGACGCTATGTACA 120  
QY 131 GCCTCTGAGTGTATGGGCTATGGGCGCCGAGCAGTTTCAGTGATGAAGTGAACACGAG 190  
DB 121 GCCTCTGAGTGTATGGGCTATGGGCGCCGAGCAGTTTCAGTGATGAAGTGAACACGAG 180  
QY 191 AACACCTGAAAGAGGGGAACACGACACTCAACCTCAGGATCCTGCAGCTCTCAGGAGG 250  
DB 181 AACACCTGAAAGAGGGGAACACGACACTCAACCTCAGGATCCTGCAGCTCTCAGGAGG 240  
QY 251 AGAGGATGAGGAGGATCTTCAGGTCAAGGGCGGAGCCCTGAAGCTGATAGCAGGAACA 310  
DB 241 AGAGGATGAGGAGGATCTTCAGGTCAAGGGCGGAGCCCTGAAGCTGATAGCAGGAACA 300  
QY 311 GGTCTACCCACAGCTGGGTGTGAGTGTGAAGATGTCTCTGATGGGCGAGATGAGACCC 370  
DB 301 GGTCTACCCACAGCTGGGTGTGAGTGTGAAGATGTCTCTGATGGGCGAGATGAGACCC 360  
QY 371 GCCAAATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAGAGCAATCAAGTGTAAAA 430  
DB 361 GCCAAATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAGAGCAATCAAGTGTAAAA 420  
QY 431 GAAGGCAAGTTGAATGATGAGGCTCTCTATGTTGGAAATTTGTTCAATAAATTC 490

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Db      421 GAAGGACGCTTGAATGATCGAGGCTCTCTATGTTGGAAATTTGTTCAATTAATCT 480
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QY      491 CCCAATAAAGCTTTACAGCTTTCTGCAAGAAAAA 530
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Db      481 CCCAATAAAGCTTTACAGCTTTCTGCAAGAAAAA 520
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RESULT 3
CF780547      517 bp mRNA linear EST 20-OCT-2003
DEFINITION AGENCOURT 15739102 NIH MGC 217 Homo sapiens cDNA clone
IMAGE:30524555 5', mRNA sequence.
ACCESSION CF780547
VERSION CF780547.1 GI:37739989
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 517)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloned by: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM604 row: e column: 12
High quality sequence stop: 517.
Location/Qualifiers
1. .517
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524555"
/tissue_type="pooled Chondrosarcoma Tumor cells"
/lab_host="NIH MGC 217"
/clone_lib="NIH MGC 217"
/notes="Vector: pYX-Asc; Site 1: EcoRI; Site 2: NotI;
Library is oligo-dT primed and directionally cloned.
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to RNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
0.5-1kb. Adaptors 5' (AATTCGGCAGCAGG)3' and 5'd
(CCTCGTGGCG)3'. 3' linker sequence - GCGGCGCTGAGAGCC T18.
Sequencing primers 3' end: T3 promoter primer 5'd
(ATTAACCTCTACTAAGGA)3'. 5' End: T7 promoter primer 5'd
(TAATACGACTACTATAGG)3'. Average insert size 0.5-1kb.
Library was constructed in the laboratory of M. Bento
Soares. Note: this is a NIH_MGC Library."

FEATURES
source
Query Match 95.2%; Score 506.6; DB 14; Length 517;
Best Local Similarity 99.2%; Pred. No. 4.1e-103;
Matches 509; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 GTGAGGACGCTGTGTGGTTCCTGCGCTCGGACCTTTTCTCTACTGAGATTCATC 64
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Db      4 GAGGGGCGAGTGTGTGGTTCCTGCGCTCGGACCTTTTCTCTACTGAGATTCATC 63
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QY      65 TGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATGCGCTAGACCAAGGCGCTA 124
|||||

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Db      64 TGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATGCGCTAGACCAAGGCGCTA 123
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|||||
Db      124 TGTACAGGCTCTCTGAATGATTTGGGCTATGCGGCCGAGCAGTTCAGTGAATGAAGTGA 183
|||||
QY      185 ACCAGCAACACTGGAAGAGGGGACCACTCAAGTCAAGGATCCCTGAGGCTGCTCA 244
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Db      184 ACCAGCAACACTGGAAGAGGGGACCACTCAAGTCAAGGATCCCTGAGGCTGCTCA 243
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QY      245 GGAGGAGGAGGATGAGGAGCATCTGCAAGTCAAGGCGCGAAGCCTGAAGCTCATAGCCA 304
|||||
Db      244 GGAGGAGGAGGATGAGGAGCATCTGCAAGTCAAGGCGCGAAGCCTGAAGCTCATAGCCA 303
|||||
QY      305 GGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGTGTCTCTGATGGGAGGAGAT 364
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Db      304 GGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGTGTCTCTGATGGGAGGAGAT 363
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QY      365 GGACCCGCCAATCCAGAGGAGTGAAGCGCTGAAGAGGTGAAGCAATCAAGTCAAGTGA 424
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Db      424 TTAAAAAGAGGCACGTTGAAATGATCGAGGCTGCTCTATGTTGAAAATTTCTTCATTAA 483
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QY      485 AATTCTCCCAATAAAGCTTTTACAGCTTCTGCA 517
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RESULT 4
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LOCUS 603392594F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5',
DEFINITION mRNA sequence.
ACCESSION BI868671
VERSION BI868671.1 GI:16042344
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 509)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloned by: Incyte Genomics, Inc.
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12026 row: 1 column: 24
High quality sequence stop: 509.
Location/Qualifiers
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/clone="IMAGE:5402663"
/tissue_type="adenocarcinoma, cell line"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
source

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ORIGIN

Query Match 92.1%; Score 490.2; DB 12; Length 509;  
Best Local Similarity 99.4%; Pred. No. 1.9e-99;  
Matches 492; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 AGCTGTGAGGAGCTGTGTGGTTCCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60  
Db 15 AGCTGTGAGGAGCTGTGTGGTTCCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 74  
Qy 61 CATCTGTGTAATATGATGTTGGCGAGAGATCGACTATATATGCGCTTAGACCAAGC 120  
Db 75 CATCTGTGTAATATGATGTTGGCGAGAGATCGACTATATATGCGCTTAGACCAAGC 134  
Qy 121 GCTATGTACAGCTCCTGAAGTGATGGCGCTATGCGCCGAGCGAGTTCAGTATGAAG 180  
Db 135 GCTATGTACAGCTCCTGAAGTGATGGCGCTATGCGCCGAGCGAGTTCAGTATGAAG 194  
Qy 181 TGGAAACAGCAACACCTGAAGAGGGGAACACGCAACTCAACGTCAGGATCCTGCAGCTG 240  
Db 195 TGGAAACAGCAACACCTGAAGAGGGGAACACGCAACTCAACGTCAGGATCCTGCAGCTG 254  
Qy 241 CTCAGGAGGAGAGATGAGGAGCATCTGAGGTCAAGGCCGAGGCTGAAGCTGATA 300  
Db 255 CTCAGGAGGAGAGATGAGGAGCATCTGAGGTCAAGGCCGAGGCTGAAGCTGATA 314  
Qy 301 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGG 360  
Db 315 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGCAGG 374  
Qy 361 AGATGGACCCGCCAAATCCAGAGAGGTGAAACGCCCTGAGAGAGGTGAAAGCAATCAC 420  
Db 375 AGATGGACCCGCCAAATCCAGAGAGGTGAAACGCCCTGAGAGAGGTGAAAGCAATCAC 434  
Qy 421 AGCTTTAAAGAGGACGCTGAATATGATGAGCTGCTCTCTTGTGGAAATTTGTTC 480  
Db 435 AGCTTTAAAGAGGACGCTGAATATGATGAGCTGCTCTCTTGTGGAAATTTGTTC 494  
Qy 481 TTAATAATCTCCCAA 495  
Db 495 TTAATAATCTCCCAA 509

RESULT 5  
AA447559/c  
LOCUS  
DEFINITION  
3' similar to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ;, mRNA  
Sequence.  
AA447559  
AA447559.1 GI:2161229  
EST.  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 489)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,  
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, J., Wyllie, J., Waterston, R., and Wilson, R.  
WashU-Merck EST Project 1997  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -41ml3 fwd. Ef from Amerisham  
High quality sequence stop: 427.

FEATURES

source

Location/Qualifiers

1..489  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:782636"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis\_NHT"  
/note="vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5']  
TGTTACCAATCTGAAGTGGGAGCGGCCCAATTTTTTTTTTTT 3']  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p773 vector. Library  
went through one round of normalization to Cots, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 89.5%; Score 476.4; DB 9; Length 489;  
Best Local Similarity 99.6%; Pred. No. 2.4e-96;  
Matches 488; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
Qy 34 CCGGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGTTGGGAGAGAT 93  
Db 489 CCGGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGAGTTGGGAGAGAT 430  
Qy 94 CGACTTATTATTTGGCCCTAGACCAAGGCGCTATGTATACAGCTCTCTGAAGTGAAT 153  
Db 429 CGACTTATTATTTGGCCCTAGACCAAGGCGCTATGTATACAGCTCTCTGAAGTGAAT 371  
Qy 154 TGGGCCCCGAGAGCTTCAGTGATGAAAGTGAACACAGCAACACCTGAAAGGGGAAAC 213  
Db 370 TGGGCCCCGAGAGCTTCAGTGATGAAAGTGAACACAGCAACACCTGAAAGGGGAAAC 311  
Qy 214 CAACCTCAACCTCAGGATCTCTGAGCTCTCAGGAGGAGAGGATGAGGAGCATCTGAG 273  
Db 310 CAACCTCAACCTCAGGATCTCTGAGCTCTCAGGAGGAGAGGATGAGGAGCATCTGAG 251  
Qy 274 GTCAAGGGCCGAAGCCCTGAAGCTGATAGCCAGGAAACAGGGGTCAACCCACAGACTGGGTGTG 333  
Db 250 GTCAAGGGCCGAAGCCCTGAAGCTGATAGCCAGGAAACAGGGGTCAACCCACAGACTGGGTGTG 191  
Qy 334 AGTGTGAAGATGTCTGTATGGGAGAGATGAGCCGCCAAATCCAGAGAGGTGAAA 393  
Db 190 AGTGTGAAGATGTCTGTATGGGAGAGATGAGCCGCCAAATCCAGAGAGGTGAAA 131  
Qy 394 CGCTCTGAAGAGTGAAGCAATCAAGTGTAAAGAGGAGGACGTTGAAATGATGAG 453  
Db 130 CGCTCTGAAGAGTGAAGCAATCAAGTGTAAAGAGGAGGACGTTGAAATGATGAG 71  
Qy 454 GCTGCTCTATGTTGGAAATTTGTCATTAATAATTTCTCCCAATAAAGCTTTACAGCCTTC 513  
Db 70 GCTGCTCTATGTTGGAAATTTGTCATTAATAATTTCTCCCAATAAAGCTTTACAGCCTTC 11  
Qy 514 TGCAGAGAAA 523  
Db 10 TGCAGAGAAA 1

RESULT 6

AW510753/c

LOCUS

DEFINITION

h39d05.x1 Soares NFL T\_GBC S1 Homo sapiens cDNA clone

IMAGE:2911881 3' similar to SW:GGE4\_HUMAN Q13068 GAGE-4 PROTEIN. ;,

mRNA sequence.

AW510753

AW510753.1 GI:7148831

EST.

SOURCE

Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 457)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
FEATURES
source
1..457
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/db_xref="taxon:9606"
/clone="IMAGE:2311881"
/lab_host="DH10B"
/clone_lib="Soares NEL T GBC S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match 85.0%; Score 452.2; DB 10; Length 457;
Best Local Similarity 99.3%; Pred. No. 6.3e-91;
Matches 454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 68 GTGAATATGAGTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGGGCTATGT 127
Db
457 GTGAATATGAGTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGGGCTATGT 398
QY 128 ACAGCTCTCTGAATGATGGGCTATGGCCCGAGCAGTTCAGTGTAGTGAAGTGAACC 187
Db
397 ACAGCTCTCTGAATGATGGGCTATGGCCCGAGCAGTTCAGTGTAGTGAAGTGAACC 338
QY 188 AGCAACCTGAGGAAGGGGAACCGCAACTCAAGCTCAGGATCTCTGCAAGTCTCAGGA 247
Db
337 AGCAACCTGAGGAAGGGGAACCGCAACTCAAGCTCAGGATCTCTGCAAGTCTCAGGA 278
QY 248 GGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGACCTGAGCTGATAGCCAGA 307
Db
277 GGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGACCTGAGCTGATAGCCAGA 218
QY 308 ACAGGTCACCCACAGACTGGGTGTGAGTGTCAAGATGGTCTGTATGGCAGGATGGA 367
Db
217 ACAGGTCACCCACAGACTGGGTGTGAGTGTCAAGATGGTCTGTATGGCAGGATGGA 158
QY 368 CCCGCAATTCAGAGGAGGTGAAACCGCTGAAGAAGGTGAAAGCAATCACAGTGTTA 427
Db
157 CCCGCAATTCAGAGGAGGTGAAACCGCTGAAGAAGGTGAAAGCAATCACAGTGTTA 98
QY 428 AAAGAAGCAGCTTGAATGATGAGGCTGCTCTATGTTGAAATTTGTTCAATTAAT 487
Db
97 AAAGAAGCAGCTTGAATGATGAGGCTGCTCTATGTTGAAATTTGTTCAATTAAT 38
QY 488 TCTCCCAATAAAGCTTTACAGCTTCTGCAAGAAAA 524
Db
37 TCTCCCAATAAAGCTTTACAGCTTCTGCAAGAAAA 1
RESULT 7

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AA738037/c
LOCUS AA738037 464 bp mRNA linear EST 22-JAN-1998
DEFINITION rx15e11.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3',
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ; mRNA sequence.
ACCESSION AA738037
VERSION AA738037.1 GI:2768794
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 464)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 511 Std Error: 0.00
Seq primer: -40md3 fwd. ET from Amersham
High quality sequence stop: 435.
FEATURES
source
1..464
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/db_xref="taxon:9606"
/clone="IMAGE:1256204"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC3"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I-
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match 83.4%; Score 443.6; DB 9; Length 464;
Best Local Similarity 98.0%; Pred. No. 5.3e-89;
Matches 449; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 75 ATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGGGCTATGACAGCT 134
Db
464 ATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGGGCTATGACAGCT 405
QY 135 CTTGAAGTGTATGGGCTTATCGGCCGAGCAGTTCAGTGTAGTGAAGTGAACCAACA 194
Db
404 CTTGAATGATTTGGGCTTATCGGCCGAGCAGTTCAGTGTAGTGAAGTGAACCAACA 345
QY 195 CTTGAAGAGGGGACACAGCAACTCAAGTCAAGATCTCGCAGCTGCTCAGGAGGAG 254
Db
344 CTTGAAGAGGGGACACAGCAACTCAAGTCAAGATCTCGCAGCTGCTCAGGAGGAG 285
QY 255 GATGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGTAGCCAGAACAGGGT 314
Db
284 GATGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGTAGCCAGAACAGGGT 225
QY 315 CACCCACAGCTGGGTGTGAGTGTGAGATGCTCTGATGGCGAGGATGACCCGCCA 374
Db
224 CACCCACAGCTGGGTGTGAGTGTGAGATGCTCTGATGGCGAGGATGACCCGCCA 165
QY 375 AATCAGAGGAGGTGAAAAACCCCTGAAGAGGTGAAAAAGCAATCACAGTGTAAAAAG 434

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Db      164 ATCCGAGAGAGTGAACGCTTGAGAGAGTGGAAGCAATCACAGTGTATTAAGAAG 105
QY      435 GCACGTGTAATGATGACGAGCTGCTCTATGTGTTGGAAAATTGTTCAATAAATCTCCCA 494
Db      104 GCACGTGTAATGATGACGAGCTGCTCTATGTGTTGGAAAATTGTTCAATAAATCTCCCA 45
QY      495 ATAAAGCTTTACAGCTTCTGCAAGAAAAGAAAAA 532
Db      44  ATAAGAGTTTACAGCCTTCTGCAAAAAGAAAAA 7

RESULT 8
AI381509/c
LOCUS   AI381509                447 bp    mRNA    linear    EST 28-MAR-1999
DEFINITION te76507.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone
IMAGE:2092597 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;,
mRNA sequence.
ACCESSION AI381509
VERSION   AI381509.1 GI:4194290
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 497 Std Error: 0.00
Seq primer: -40Up from Gibco.
Location/Qualifiers
FEATURES
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/clone_lib="Soares_NFL_T_QBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 83.1%; Score 442.2; DB 9; Length 447;
Best Local Similarity 99.3%; Pred. No. 1.le-88;
Matches 444; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      79 GTTCGCGAGGAGATCGACCTATTATTCGCTAGACCAAGCGCTATGACAGCTCTCTG 138
Db      447 GTTCGCGAGGAGATCGACCTATTATTCGCTAGACCAAGCGCTATGACAGCTCTCTG 388
QY      139 AAGTGATTTGGCGCTATGCGGCCGAGCGAGTTTCAGTGATGAAGTGAACCAACACCTG 198
Db      387 AAATGATTTGGCGCTATGCGGCCGAGCGAGTTTCAGTGATGAAGTGAACCAACACCTG 328
QY      199 AAGAAGGGGAACCAACCACTCAACGTCCAGGATCTTCGAGCTCTCAGGAGGAGGATG 258
Db      327 AAGAAGGGGAACCAACCACTCAACGTCCAGGATCTTCGAGCTCTCAGGAGGAGGATG 268

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QY      259 AGGGAGCATCTGCAGGTCAAGGCCGGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACC 318
Db      267 AGGGAGCATCTGCAGGTCAAGGCCGGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACC 208
QY      319 CACAGACTGGGTGTGATGTGAAGATGGTCTCTGATCGGCAGGAGATGGACCCGCAATC 378
Db      207 CACAGACTGGGTGTGATGTGAAGATGGTCTCTGATCGGCAGGAGATGGACCCGCAATC 148
QY      379 CAGAGGAGGTGAACACGCTGGAAGAAGTGAAGCAATCACAGTGTGTAAGAAAGAGGCAC 438
Db      147 CAGAGGAGGTGAACACGCTGGAAGAAGTGAAGCAATCACAGTGTGTAAGAAAGAGGCAC 88
QY      439 GTTGAATGATGACAGCTGCTCTATGTTGGAATTTGTTCAATAAATCTCCCAATAA 498
Db      87 GTTGAATGATGACAGCTGCTCTATGTTGGAATTTGTTCAATAAATCTCCCAATAA 28
QY      499 AGCTTTACAGCCTTCTGCAAGAAAAA 525
Db      27 AGCTTTACAGCCTTCTGCAAGAAAAA 1

RESULT 9
BG120336
LOCUS   BG120336                480 bp    mRNA    linear    EST 30-JAN-2001
DEFINITION 602353732F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4451958 5',
mRNA sequence.
ACCESSION BG120336
VERSION   BG120336.1 GI:12613845
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0239 row: p column: 07
High quality sequence stop: 480.
Location/Qualifiers
FEATURES
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1..480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4451958"
/tissue_type="adenocarcinoma, cell line"
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/clone_lib="NIH_MGC_90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 82.4%; Score 438.6; DB 12; Length 480;
Best Local Similarity 99.1%; Pred. No. 7e-88;
Matches 441; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      88 GAAGATCGACCTATTATTCGCTAGACCAAGCGCTATGATACGCTCTCGAAGTGATG 147
Db      1 GAAGATCGACCTATTATTCGCTAGACCAAGCGCTATGATACGCTCTCGAAGTGATG 60

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QY 148 GGCCTATGCGCCGAGCAGTTCAGTGATGAAGTGAACACAGCAACACCTGAGAGGG 207  
Db 61 GGCCTATGCGCCGAGCAGTTCAGTGATGAAGTGAACACAGCAACACCTGAGAGGG 120  
QY 208 AACACGAACTCAACGTCAGGATCCTGACGCTGCTCAGGAGGAGAGGATGAGGAGCAT 267  
Db 121 AACACGAACTCAACGTCAGGATCCTGACGCTGCTCAGGAGGAGAGGATGAGGAGCAT 180  
QY 268 CTGCGAGTCAAGGCGGAGACCTGAAGCTGATAGCCAGGAACAGGTCACCCACAGACTG 327  
Db 181 CTGCGAGTCAAGGCGGAGACCTGAAGCTGATAGCCAGGAACAGGTCACCCACAGACTG 240  
QY 328 GGTGTGAGTGAAGATGCTCTGATGGCGAGAGATGACCGCCAAATCCAGAGGAG 387  
Db 241 GGTGTGAGTGAAGATGCTCTGATGGCGAGAGATGACCGCCAAATCCAGAGGAG 300  
QY 388 TGAACACGCTCAAGAGGTGAAGAGCAATCAAGTGTAAAGAGGACACGTTGAAATG 447  
Db 301 TGAACACGCTCAAGAGGTGAAGAGCAATCAAGTGTAAAGAGGACACGTTGAAATG 360  
QY 448 ATGCGAGTCTCTATGCTGAAATTTGTTCAATTAATTTCCCAATAAGCTTTTACA 507  
Db 361 ATGCGAGTCTCTATGCTGAAATTTGTTCAATTAATTTCCCAATAAGCTTTTACA 420  
QY 508 GCCTTCTGCAAGAAAAA 532  
Db 421 GCCTTCTGCAAGAAAAA 445

RESULT 10  
LOCUS CB115693  
DEFINITION K-EST0159805 L8SK0 Homo sapiens CDNA clone L8SK0-8-B09 5', mRNA  
sequence.  
ACCESSION CB115693  
VERSION CB115693.1 GI:27941500  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 505)  
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.  
TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 8 row: B column: 09  
High quality sequence stop: 505.  
FEATURES  
Location/Qualifiers  
1..505  
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/db\_xref="taxon:9606"  
/clone="L8SK0-8-B09"  
/sex="M"  
/cell\_line="SCK"  
/lab\_host="Top10F"  
/clone\_lib="L8SK0"  
/note="Organ: Liver; Vector: pVT3-Pac; Site 1: EcoRI;  
Site 2: NotI; The library was contributed by the Soares  
laboratory and it was constructed as described by Bonaldo,  
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research  
6(9): 791-806. RNA was prepared from harvested cell  
culture."

Query Match 82.0%; Score 436; DB 14; Length 505;  
Best Local Similarity 97.8%; Pred. No. 2.7e-87;  
Matches 442; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 23 GTTCTGCGCTCGGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGATTTG 82  
Db 19 GGTCTGCGCTCGGACTCTTTTCTCTACTGAGATTCATCTGTGTAATATGATTTG 78  
QY 83 GCGAGGAATCGACTTATTATTGGCTAGACCAAGGCGCTATGTACAGCTCCTGAAGT 142  
Db 79 GCGAGGAATCGACTTATTATTGGCTAGACCAAGGCGCTATGTACAGCTCCTGAAGT 138  
QY 143 GATTGGGCTATGCGGCGGAGCAGTTCAGTGAATGGAACACGCAACACCTGAAGA 202  
Db 139 GATTGGGCTATGCGGCGGAGCAGTTCAGTGAATGGAACACGCAACACCTGAAGA 198  
QY 203 AGGGGAACAGCAACTCAACGTCAGGATCCTGCACTGCTCAGGAGGAGAGATGAGG 262  
Db 199 AGGGGAACAGCAACTCAACGTCAGGATCCTGCACTGCTCAGGAGGAGAGATGAGG 258  
QY 263 AGCATCTGAGGTCAAGGCGGAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACA 322  
Db 259 AGCATCTGAGGTCAAGGCGGAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACA 318  
QY 323 GACTGGGTGAGTGTGAAGATGTCCTGATGGGAGGAGATGACCCGCAAAATCCAGA 382  
Db 319 GACTGGGTGAGTGTGAAGATGTCCTGATGGGAGGAGATGACCCGCAAAATCCAGA 378  
QY 383 GGAGGTGAAGAGCGCTGAGAGGTGAAGCAATCAGTGTAAAGAGGACGCTTG 442  
Db 379 GGAGGTGAAGAGCGCTGAGAGGTGAAGCAATCAGTGTAAAGAGGACGCTTG 438  
QY 443 AAATGATCAGGCTGCTCTATGTTGAAAT 474  
Db 439 AAATGATCAGGCTGCTCTATGTTGAAAT 470

RESULT 11  
LOCUS AA760996  
DEFINITION nx32h08.s1 NCI CGAP GC4 Homo sapiens CDNA clone IMAGE:1257855 3'  
similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. i, mRNA sequence.  
ACCESSION AA760996  
VERSION AA760996.1 GI:2809926  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 450)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Sequencing by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 331.  
FEATURES  
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1..450  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1257855"

/tissue type="pooled germ cell tumors"

/lab host="DH10B"  
/clone lib="NCI CGAP GC4"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified p773  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 81.1%; Score 431.6; DB 9; Length 450;  
Best Local Similarity 98.7%; Pred. No. 2.6e-86;  
Matches 445; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
  
QY 75 ATGAGTTGGCGAGGAGATCGACTATTATTGGCTAGACCAAGCGCTATGACGCT 134  
Db 450 ATGAGTTGGCGAGGAGATCGACTATTATTGGCTAGACCAAGCGCTATGACGCT 391  
  
QY 135 CCTGAAGTATTGGGCTATGCGCCCGAGCGCTTCAGTGTGAAGTGGACCAACA 194  
Db 390 CCTGAAGTATTGGGCTATGCGCCCGAGCGCTTCAGTGTGAAGTGGACCAACA 331  
  
QY 195 CCTGAAGTATTGGGCTATGCGCCCGAGCGCTTCAGTGTGAAGTGGACCAACA 254  
Db 330 CCTGAAGTATTGGGCTATGCGCCCGAGCGCTTCAGTGTGAAGTGGACCAACA 271  
  
QY 255 GATGAGGAGCATCTGCAGTCAAGGCCGGAAGCCTGAAGCTGATGACCAAGCAAGG 314  
Db 270 GATGAGGAGCATCTGCAGTCAAGGCCGGAAGCCTGAAGCTGATGACCAAGCAAGG 211  
  
QY 315 CACCCAGACTGGTGTGAGTGTGAAGTGTGCTGATGGCGAGGAGTGGACCCGCA 374  
Db 210 CACCCAGACTGGTGTGAGTGTGAAGTGTGCTGATGGCGAGGAGTGGACCCGCA 151  
  
QY 375 AATCCAGAGGAGTGAAGAGCGCTGGAAGAGGTGAAAGCAATCACAGTGTGAAAGAG 434  
Db 150 AATCCAGAGGAGTGAAGAGCGCTGGAAGAGGTGAAAGCAATCACAGTGTGAAAGAG 91  
  
QY 435 GCAGTTGAATGATGACGAGTGTCTCTATGTTGGAAATTTGTTCAATAAATCTCCCA 494  
Db 90 ACAGTTGAATGATGACGAGTGTCTCTATGTTGGAAATTTGTTCAATAAATCTCCCA 31  
  
QY 495 ATAAAGCTTTACAGCTTCTGCAAGAAAA 525  
Db 30 ATAAAG-TTTACAGCTTCTGCAAGAAAA 1

RESULT 12  
AI187350/c  
LOCUS  
DEFINITION  
qt29405.x1 Soares testis\_NHT Homo sapiens cDNA clone IMAGE:1751408  
3', similar to SW:GGE4\_HUMAN Q13068 GAGE-4 PROTEIN. [1] ;, mRNA  
sequence.  
ACCESSION  
AI187350  
VERSION  
AI187350.1 GI:3737988  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 455)  
AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert length: 504 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 391.

## FEATURES

## source

1. .455  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1751408"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis\_NHT"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5].  
TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'.  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p773 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 78.4%; Score 417; DB 9; Length 455;  
Best Local Similarity 97.4%; Pred. No. 4.8e-83;  
Matches 445; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
  
QY 75 ATGAGTTGGCGAGGAGATCGACTATTATTGGCTAGACCAAGCGCTATGACGCT 134  
Db 455 ATGAGTTGGCGAGGAGATCGACTATTATTGGCTAGACCAAGCGCTATGACGCT 398  
  
QY 135 CCTGAAGTATTGGGCTATGCGCCCGAGCGCTTCAGTGTGAAGTGGACCAACA 194  
Db 397 CCTGAAGTATTGGGCTATGCGCCCGAGCGCTTCAGTGTGAAGTGGACCAACA 338  
  
QY 195 CCTGAAGAGGGGAACAGCACTCAACGTGAGATCCTGAGTGTGAGGAGGAG 254  
Db 337 CCTGAAGAGGGGAACAGCACTCAACGTGAGATCCTGAGTGTGAGGAGGAG 278  
  
QY 255 GATGAGGAGCATCTGCAGTCAAGGCCGGAAGCCTGAAGCTGATGACCAAGCAAGG 314  
Db 277 GATGAGGAGCATCTGCAGTCAAGGCCGGAAGCCTGAAGCTGATGACCAAGCAAGG 218  
  
QY 315 CACCCAGACTGGTGTGAGTGTGAAGTGGTCTCTGATGGCGAGGAGTGGACCCGCA 374  
Db 217 CACCCAGACTGGTGTGAGTGTGAAGTGGTCTCTGATGGCGAGGAGTGGACCCGCA 158  
  
QY 375 AATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAAGCAATCACAGTGTGAAAGAG 434  
Db 157 AATCCAGAGGAGTGAAGAGCGCTGAAGAGGTGAAAGCAATCACAGTGTGAAAGAG 98  
  
QY 435 GCAGTTGAATGATGACGAGTGTCTCTATGTTGGAAATTTGTTCAATAAATCTCCCA 494  
Db 97 ACAGTTGAATGATGACGAGTGTCTCTATGTTGGAAATTTGTTCAATAAATCTCCCA 38  
  
QY 495 ATAAAGCTTTACAGCTTCTGCAAGAAAA 531  
Db 37 ATAAAGCTTTACAGCTTCTGCAAGAAAA 1

## RESULT 13

## AW016546/c

## LOCUS

## DEFINITION

## AW016546

## ACCESSION

## VERSION

AW016546  
UT-H-BIOP-abg-g-06-0-UI.s1 NCI CGAP\_Sub2 Homo sapiens cDNA clone  
IMAGE:2711986 3', mRNA sequence.  
AW016546  
AW016546.1 GI:5865303

linear EST 10-SEP-1999

```

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP Sub2 library is a subtracted library derived from
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward
POLYA=Yes.

FEATURES             Location/Qualifiers
     source          1..418
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2711986"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_Sub2"
                     /note="Vector: pT7D3-Pac (Pharmacia) with a modified
                     polylinker; Site 1: Not I; Site 2: Eco RI; The
                     NCI_CGAP Sub2 library is a subtracted library derived from
                     BL-1 constitutes a mixture of 21 normalized or
                     subtracted NCI_CGAP libraries: NCI_CGAP Co4,
                     NCI_CGAP Pr22, NCI_CGAP Pr28, NCI_CGAP Co10,
                     NCI_CGAP Co16, NCI_CGAP Kid3, NCI_CGAP Kid12,
                     NCI_CGAP Kid3, NCI_CGAP Kid11, NCI_CGAP Lym2,
                     NCI_CGAP Br2, NCI_CGAP Co8, NCI_CGAP CL11, NCI_CGAP_Lei2,
                     NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
                     NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6, NCI_CGAP_Brn25.
                     These 21 libraries were pooled and a single-stranded DNA
                     preparation of the resulting mixture was used as a tracer
                     in a subtractive hybridization with a driver whose
                     composition is detailed below: NCI_CGAP Kid3 pool 1 LLAM
                     3334-3337, 3682-3683, 3798-3803 (IMAGE Clones
                     132376-132391, 1456008-1456775, 1500552-1502855)
                     NCI_CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
                     (IMAGE Clones 1323912-1325831, 1471368-1472903,
                     1492104-1493255) NCI_CGAP Lu5 pool 1 LLAM 3575-3582,
                     3851-3854 (IMAGE Clones 1414920-1417991,
                     1520904-1522439) NCI_CGAP_GC4 pool 1 LLAM 3164-3167,
                     3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631,
                     1469064-1470983, 1475592-1476743) NCI_CGAP Pr22 pool 1
                     LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones
                     985608-986759, 1101192-1101959, 1217928-1220615)
                     NCI_CGAP Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
                     Clones 1057416-1061255, 1144584-1145351) The resulting
                     subtracted library contained 4 million recombinants.
                     Subtraction was performed as previously described
                     [Bonaldi, Lennon & Soares (1996): Normalization and
                     Subtraction: Two Approaches To Facilitate Gene Discovery.
                     Genome Research 6, 791-806.
                     TAG TISSUE=germ cell
                     TAG_LIB=NCI_CGAP_GC4
                     TAG_SEQ=AAATC"

ORIGIN
Query Match          76.6%; Score 407.4; DB 9; Length 418;
Best Local Similarity 98.6%; Pred. No. 6.8e-81;
Matches 411; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 116 AAGCGCTATGACAGCTCTCTGAAGTGAATGGGCTATGGCGCCGAGCAGTTCAGTGA 175
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

Db 418 AAGCGCTACGTAGAGCTCTGAAATGATTTGGGCTATGGCGCCGAGCAGTTCAGTGA 359
QY 176 TGAAGTGAACACAGCAACACCTGAAGAAAGGGGAACCAACACTCAACGTCAGGATCTCTGC 235
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 TGAAGTGAACACAGCAACACCTGAAGAAAGGGGAACCAACACTCAACGTCAGGATCTCTGC 299
QY 236 AGCTGCTCAGAGGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGCCGAGCCCTGAAGC 295
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 298 AGCTGCTCAGAGGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGCCGAGCCCTGAAGC 239
QY 296 TGATAGCCAGCAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGG 355
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 TCATAGCCAGCAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGG 179
QY 356 GCAGGAGATGACCCCGCCAAATCCAGAGAGGTGAAAACGCTGAAAGAGGTGAAAAAGCA 415
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 GCAGGAGATGACCCCGCCAAATCCAGAGAGGTGAAAACGCTGAAAGAGGTGAAAAAGCA 119
QY 416 ATCAGAGTGTAAAGAAAGGACCGTTGAAATGATCAGGCTGCTCTATGTGGAAATTT 475
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 118 ATCAGAGTGTAAAGAAAGGACCGTTGAAATGATCAGGCTGCTCTATGTGGAAATTT 59
QY 476 GTTCATTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAGAAAAA 532
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 GTTCATTAAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAGAAAAA 2

RESULT 14
AA868226/c
LOCUS AA868226
DEFINITION ak4807.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1409245
3' similar to SW:GGE2_HUMAN Q13066 GAGE-2 PROTEIN. [1] ;, mRNA
sequence.
ACCESSION AA868226
VERSION AA868226.1 GI:2963671
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 426)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA library preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 363.
Location/Qualifiers
     source          1..426
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1409245"
                     /sex="male"
                     /lab_host="DH10B"
                     /clone_lib="Soares testis NHT"
                     /note="Vector: pT7D3-Pac (Pharmacia) with a modified
                     polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech
                     Laboratories, Inc., and primed with a Not I - oligo(dT)
                     primer [5].
                     TGTTACCAATCTGAAGTGGGAGCGCGCCCAATTTTTTTTTTTT 3'].

```

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

```

Query Match      75.0%; Score 398.8; DB 9; Length 426;
Best Local Similarity 96.7%; Pred. No. 5.7e-79;
Matches 406; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 102 TATTGGCCTAGACCAAGCGCCTATGTACAGCCTCTCTGAAAGTGAATGGGCTTATCGCGCCC 161
    |||
Db 420 TATCGGCCTAGACCAAGCAGCTAGTAGAGCCTCTCTGAAATGNANTTGGCTATGCGGCC 361

QY 162 GAGCAGTTCACTGATGAAGTGGACACAGCAACCACTTGAAAGAGGGACAGCAACTCAA 221
    |||
Db 360 GAGCAGTTCACTGATGAAGTGGACACCACTTGAAAGAGGGACAGCAACTCAA 301

QY 222 CGTCAGGATCCTGAGCTGCTCAGGAGGGAGAGGATGAGGAGCATCTGCAGGTCAGAGG 281
    |||
Db 300 CGTCAGGATCCTGAGCTGCTCAGGAGGGAGAGGATGAGGAGCATCTGCAGGTCAGAGG 241

QY 282 CCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGGAA 341
    |||
Db 240 CCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGGAA 181

QY 342 GATGGTCTCATGGGAGGAGATGGCCGCCAAATCCAGAGGAGTGAAGAGCGCTGAA 401
    |||
Db 180 GATGGTCTCATGGGAGGAGATGGCCGCCAAATCCAGAGGAGTGAAGAGCGCTGAA 121

QY 402 GAAGGTGAAAGCAATCACAGTGTGTTAAAGAGGACAGCTTGAATGATGAGGCTGCTCC 461
    |||
Db 120 GAAGGTGAAAGCAATCACAGTGTGTTAAAGAGGACAGCTTGAATGATGAGGCTGCTCC 61

QY 462 TATGTTGGAATTTGTTCAATTAATTTCTCCCAATAAGCTTTACAGCCTTCTGCAAGA 521
    |||
Db 60 TATGTTGGAATTTGTTCAATTAATTTCTCCCAATAAGCTTTACAGCCTTCTTCAAAA 1

```

## RESULT 15

```

BM836228
LOCUS      383 bp      mRNA      linear      EST 06-MAR-2002
DEFINITION K-EST0111762 S5SNU484s1 Homo sapiens cDNA clone S5SNU484s1-15-D07
5', mRNA sequence.

```

```

ACCESSION  BM836228
VERSION     BM836228.1 GI:19192637
KEYWORDS   EST.
SOURCE     Homo sapiens (human)

```

## ORGANISM

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 383)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 15 row: D column: 07
High quality sequence stop: 383.
Location/Qualifiers
1..383
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S5SNU484s1-15-D07"

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## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

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## source

## source

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## source

## source

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## source

## source

## source

## source

## source

```

/sex="M"
/tissue_type="Stomach"
/cell_type="Epithelial"
/cell_line="SNU-484"
/lab_host="Top10F"
/clone_lib="S5SNU484s1"

```

```

/notes="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was decapped with tobacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dT-selected
mRNA by priming with dT-tailed vector. The dT-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with E. coli DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
After analyzing and sequencing about 2,000 ~ 3,000
colonies in original cDNA library, the abundant cDNAs were
selected and amplified by PCR reaction using vector region
primer including T7 promoter as 5' primer and N(dT)14 as
3' primer. The PCR products were used as template for
synthesis of biotinylated single stranded RNA by in vitro
transcription reaction. The synthesized RNA probes were
hybridized with antisense single stranded cDNAs prepared
from original library and incubated with avidin-gel.
After removing DNA-RNA hybrids by centrifuge, the
subtracted cDNA libraries were constructed by
transformation of the remaining DNA into competent cells E.
coli Top10F' with electroporation method."

```

## ORIGIN

```

Query Match      71.0%; Score 377.8; DB 12; Length 383;
Best Local Similarity 99.5%; Pred. No. 2.9e-74;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 62 ATCTGTGTGAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGACCAAGGCG 121
    |||
Db 3 ATCTGTGTGAATATGAGTTGGCGAGAGATCGACCTATTATTGGCCTAGACCAAGGCG 62

QY 122 CTATGTACAGCCTCTGAGTGAATGATTGGGCTATCGGCCCCGAGCAGTTCAGTGAAGT 181
    |||
Db 63 CTATGTACAGCCTCTGAGTGAATGATTGGGCTATCGGCCCCGAGCAGTTCAGTGAAGT 122

QY 182 GGAACCAAGCAACACCTGAAGAAGGGAAACAGCAACTCAACGTCAGGATCCTGCAGCTGC 241
    |||
Db 123 GGAACCAAGCAACACCTGAAGAAGGGAAACAGCAACTCAACGTCAGGATCCTGCAGCTGC 182

QY 242 TCAGGAGGGAGAGGATGAGGAGCATCTGCAGTCAAGGCCCGAAGCCTGAAGCTGTAG 301
    |||
Db 183 TCAGGAGGGAGAGGATGAGGAGCATCTGCAGTCAAGGCCCGAAGCCTGAAGCTGTAG 242

QY 302 CCGAGGACAGGTCACCCACAGACTGGTGTGAGTGTGAAGATGCTCTCATGGGCGAGGA 361
    |||
Db 243 CCGAGGACAGGTCACCCACAGACTGGTGTGAGTGTGAAGATGCTCTCATGGGCGAGGA 302

QY 362 GATGGACCCGCCAAATCCAGAGGAGTGAAGAAACGCTTGAAGAGGTTCAAAAGCAATCACA 421
    |||
Db 303 GATGGACCCGCCAAATCCAGAGGAGTGAAGAAACGCTTGAAGAGGTTCAAAAGCAATCACA 362

QY 422 GTGTAAAGAGAGGCGAGTTTG 442
    |||
Db 363 GTGTAAAGAGAGGCGAGTTTG 383

```

Search completed: August 6, 2004, 20:52:27

Job time : 2417 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 18:20:25 ; Search time 333 Seconds

(without alignments)  
6786.911 Million cell updates/sec

Title: US-09-782-745-17

Perfect score: 532

Sequence: 1 AGCTGTGAGGCGAGTGTGTG.....CTCCAGAGAAAAA 532

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 4998588

Minimum DB seq length: 0

Maximum DB seq length: 532

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001s:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002s:\*

7: Geneseqn2003as:\*

8: Geneseqn2003bs:\*

9: Geneseqn2003cs:\*

10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	532	100.0	532	2	AAX90522 GAGE-5 tu
2	524	98.5	532	2	AAX18720
3	517.4	97.3	528	6	ABL66323 Lung canc
4	515.8	97.0	527	7	ACC51027 Human bla
5	515.8	97.0	527	7	ABX76236 Lung canc
6	508.8	95.6	526	7	ADA15802 Human GAG
7	504.4	94.8	528	7	ADA15801 Human GAG
8	496.8	93.4	530	7	ABZ20463
9	350.8	65.9	430	3	AAC02129 Human sec
10	304.6	57.3	530	4	AAS60104 Human can
11	302.4	56.8	365	4	AAS60496 Human can
12	237	44.5	277	7	ABZ19551 Group III
13	235.4	44.2	257	7	ABZ19555 Group III
14	235.4	44.2	264	7	ABZ19755 Group III
15	227.4	42.7	229	7	ABZ20497
16	227	42.7	227	7	ABZ20480
17	226	42.5	229	7	ABZ18686 Group III
18	211.4	39.7	259	7	ABZ19791 Group III
19	208.4	39.2	520	7	ABT15737 Human can
20	204	38.3	225	7	ABZ19533 Group III
21	200.8	37.7	509	7	ABX77605 Different
22	200.8	37.7	509	8	ACD42232 Human GAG
23	200.8	37.7	509	9	ADC24646 Human cDN

## ALIGNMENTS

RESULT 1	
AAX90522	
ID	AAX90522 standard; cDNA; 532 BP.
XX	
AC	AAX90522;
XX	
DT	30-SEP-1999 (first entry)
XX	
DE	GAGE-5 tumour rejection antigen clone nucleotide sequence.
XX	
KW	Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;
KW	therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;
KW	GAGE; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9937665-A1.
XX	
PD	29-JUL-1999.
XX	
PF	12-JAN-1999; 99WO-US000775.
XX	
PR	23-JAN-1998; 98US-00012818.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;
XX	
DR	WPI; 1999-469111/39.
XX	
PT	New isolated peptides which bind to HLA-A29 molecules, which are tumor
PT	rejection antigens used for detection and therapy of pathological
PT	conditions, e.g. cancer.
XX	
PS	Example 13; Fig 4; 62pp; English.
XX	
CC	The present invention describes peptides which bind to human leukocyte
CC	antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into
CC	tumour rejection antigens. They can be used for detecting cytolytic T
CC	lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-
CC	typing assays. Complexes of HLA-29 molecules and the peptides can be used
CC	for stimulating CTLs in vivo. The present sequence represents a GAGE
CC	tumour rejection antigen clone, from an example from the present
CC	invention
XX	
SQ	Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 U; 0 Other;

24	183.6	34.5	532	4	AAI60530	Aai60530 Human pol
25	171	32.1	219	7	ABZ19538	Abz19538 Group III
26	164.2	30.9	503	5	AAS69484	Aas69484 DNA encod
27	140	26.3	528	7	ABT15728	Abt15728 Human can
28	133.2	25.0	475	4	AAI14981	Aai14981 Human NOV
29	108	20.3	399	5	AAF68151	Aaf68151 Human lun
30	108	20.3	399	6	ABK38062	Abk38062 cDNA enco
31	108	20.3	399	7	ACA10391	Aca10391 Human lun
32	108	20.3	399	7	ABX99342	Abx99342 Lung canc
33	108	20.3	399	10	ADR72125	Ade72125 Human lun
34	103.6	19.5	505	6	AAD24228	Aad24228 Human dif
35	103.4	19.4	463	6	ABA92217	Aba92217 Melanoma
36	101.6	19.1	515	4	AAS93807	Aas93807 Human pro
37	101.6	19.1	515	4	AAS63900	Aas63900 Human pro
38	101.6	19.1	515	4	AAH02872	Aah02872 Prostate
39	101.6	19.1	515	4	AAH85121	Aah85121 Human pro
40	101.6	19.1	515	5	ACA59708	Aca59708 Prostate
41	101.6	19.1	515	6	ABL95271	Ab195271 Human P10
42	101.6	19.1	515	7	ACC95435	Acc95435 Prostate
43	101.6	19.1	515	9	ADB13922	Adb13922 Human pro
44	100.8	18.9	214	4	AAS24637	Aas24637 Human ova
45	100.8	18.9	320	5	AAH83260	Aah83260 Human ova



ABL66323	ABL66323 standard; DNA; 528 BP.
XX	ABL66323
XX	ABL66323
XX	ABL66323
XX	15-MAY-2002 (first entry)
DT	
XX	Lung cancer related gene sequence SEQ ID NO:4660.
XX	
XX	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW	gene; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO2001194629-A2.
XX	
PD	13-DEC-2001.
XX	
PF	30-MAY-2001; 2001WO-US010838.
XX	
PR	05-JUN-2000; 2000US-0209473P.
PR	05-JUN-2000; 2000US-0209531P.
PR	18-SEP-2000; 2000US-0233133P.
PR	18-SEP-2000; 2000US-0233617P.
PR	20-SEP-2000; 2000US-0234009P.
PR	20-SEP-2000; 2000US-0234034P.
PR	20-SEP-2000; 2000US-0234052P.
PR	22-SEP-2000; 2000US-0234509P.
PR	22-SEP-2000; 2000US-0234567P.
PR	23-SEP-2000; 2000US-0234923P.
PR	25-SEP-2000; 2000US-0234924P.
PR	25-SEP-2000; 2000US-0235077P.
PR	25-SEP-2000; 2000US-0235082P.
PR	25-SEP-2000; 2000US-0235134P.
PR	25-SEP-2000; 2000US-0235280P.
PR	26-SEP-2000; 2000US-0235637P.
PR	26-SEP-2000; 2000US-0235638P.
PR	27-SEP-2000; 2000US-0235711P.
PR	27-SEP-2000; 2000US-0235720P.
PR	27-SEP-2000; 2000US-0235840P.
PR	27-SEP-2000; 2000US-0235863P.
PR	28-SEP-2000; 2000US-0236028P.
PR	28-SEP-2000; 2000US-0236032P.
PR	28-SEP-2000; 2000US-0236033P.
PR	28-SEP-2000; 2000US-0236034P.
PR	28-SEP-2000; 2000US-0236109P.
PR	28-SEP-2000; 2000US-0236111P.
PR	29-SEP-2000; 2000US-0236842P.
PR	29-SEP-2000; 2000US-0236891P.
PR	02-OCT-2000; 2000US-0237172P.
PR	02-OCT-2000; 2000US-0237173P.
PR	02-OCT-2000; 2000US-0237278P.
PR	02-OCT-2000; 2000US-0237294P.
PR	02-OCT-2000; 2000US-0237295P.
PR	02-OCT-2000; 2000US-0237316P.
PR	03-OCT-2000; 2000US-0237425P.
PR	03-OCT-2000; 2000US-0237598P.
PR	03-OCT-2000; 2000US-0237604P.
PR	03-OCT-2000; 2000US-0237606P.
PR	03-OCT-2000; 2000US-0237608P.
PR	01-NOV-2000; 2000US-0244867P.
PR	01-NOV-2000; 2000US-0245084P.
XX	
PA	(AVAL-) AVALON PHARM.
XX	
PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI	Soppet DR, Weaver Z;
XX	
DR	WPI; 2002-188264/24.
XX	
PT	Screening for anti-neoplastic agent involves exposing cells to a chemical





CC for treating lung cancer, such as small cell lung cancer, non-small cell  
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
CC for diagnostic purposes and as targets for screening for therapeutic  
CC compounds that modulate lung cancer, such as antibodies. Sequences  
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the  
CC invention  
XX  
SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 97.0%; Score 515.8; DB 7; Length 527;  
Best Local Similarity 99.6%; Pred. No. 2.7e-137;  
Matches 517; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGCTGTGAGGCGAGTCTGTGGTTCCTCGCGTCGGGACTCTTTTCTCTACTCAGATT 60  
DB |||||  
DB 8 AGCTGTGAGGCGAGTCTGTGGTTCCTCGCGTCGGGACTCTTTTCTCTACTCAGATT 67  
QY 61 CATCTGTGAAATATGATGTGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGGC 120  
DB |||||  
DB 68 CATCTGTGAAATATGATGTGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGGC 127  
QY 121 GCTATGTACAGCTCTCTGAAGTATTGGGCTATCGGCCCGAGCAGTTCAGTGATGAAG 180  
DB |||||  
DB 128 GCTATGTACAGCTCTCTGAAGTATTGGGCTATCGGCCCGAGCAGTTCAGTGATGAAG 187  
QY 181 TGGAAACCAACACCTCTGAAGGAGGGAACCAAGCAACTCAAGTCAGGATCTCGAGCTG 240  
DB |||||  
DB 188 TGGAAACCAACACCTCTGAAGGAGGGAACCAAGCAACTCAAGTCAGGATCTCGAGCTG 247  
QY 241 CTCAGGAGGAGATGAGGAGATCTGCAAGTCAAGGCCGAGGCTGAGCTGATA 300  
DB |||||  
DB 248 CTCAGGAGGAGATGAGGAGATCTGCAAGTCAAGGCCGAGGCTGAGCTGATA 307  
QY 301 GCCAGGAACAGGTCACCCACAGACTGGGTGAGTGAGTGAAGATGCTCTGATGGCAGG 360  
DB |||||  
DB 308 GCCAGGAACAGGTCACCCACAGACTGGGTGAGTGAGTGAAGATGCTCTGATGGCAGG 367  
QY 361 AGATGGACCGCCCAATCCAGAGGAGGTGAACCGCTGAAGAGGTGAAGAGCAATCAC 420  
DB |||||  
DB 368 AGGTGACCCGCCCAATCCAGAGGAGGTGAACCGCTGAAGAGGTGAAGAGCAATCAC 427  
QY 421 AGTGTAAAGAGGACGCTGAAATGATGCAAGGCTGCTCTATGTTGAAATTTGTTCA 480  
DB |||||  
DB 428 AGTGTAAAGAGGACACGCTTGAATGATGCAAGGCTGCTCTATGTTGAAATTTGTTCA 487  
QY 481 TTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAA 519  
DB |||||  
DB 488 TTAATAATCTCCCAATAAGCTTTTACAGCTTCTGCAAA 526

## RESULT 6

ID ADA15802 standard; cDNA; 526 BP.  
XX  
AC ADA15802;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human GAGE-7B cDNA.  
XX  
KW Human; GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL;  
KW human leukocyte antigen; HLA; tumour rejection antigen precursor;  
KW major histocompatibility complex; MHC; cytolytic T cell proliferation;  
KW chromosome Xp11.2-p11.4.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 55..408  
FT /\*tag= a

/product= "Human GAGE-7B"  
/transl\_except= (pos:115..162, aa: GPMRPEQSGSDEVPEMI)  
/transl\_except= (pos:265..306, aa: HPQTKPRAHSQEQ)  
US6509172-B1.  
PD 21-JAN-2003.  
XX  
PF 30-SEP-1998; 98US-00163748.  
XX  
PR 30-SEP-1998; 98US-00163748.  
XX (LUDW-) LUDWIG INST CANCER RES.  
PI De Backer O, Van Den Eynde B, Boon-Falleur T;  
XX  
DR WPI; 2003-401119/38.  
XX P-PSDB; ADA15777.  
PT New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor  
PT rejection antigen precursors, which complex to major histocompatibility  
PT complex molecules to facilitate the proliferation of cytolytic T cells.  
XX  
PS Claim 1; Col 9-10; 15pp; English.  
CC The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the  
CC nucleic acid molecules encoding them. The invention also relates to an  
CC expression vector comprising an isolated nucleic acid molecule of the  
CC invention operably linked to a promoter, a recombinant cell comprising  
CC the isolated nucleic acid molecule or the expression vector and an  
CC expression kit useful in generating cytolytic T lymphocytes (CTLs) or  
CC determining if CTLs are present in a sample comprising the isolated  
CC nucleic acid molecule and the isolated nucleic acid that encodes a human  
CC leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid  
CC molecules encode tumour rejection antigen precursors, which complex to  
CC major histocompatibility complex (MHC) molecules to facilitate the  
CC proliferation of cytolytic T cells. This sequence represents cDNA  
CC encoding the human GAGE-7B polypeptide of the invention. The gene resides  
CC on chromosome Xp11.2-p11.4.  
XX  
SQ Sequence 526 BP; 168 A; 109 C; 143 G; 106 T; 0 U; 0 Other;

Query Match 95.6%; Score 508.8; DB 7; Length 526;  
Best Local Similarity 99.6%; Pred. No. 2.9e-137;  
Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 21 TGGTTCCTCGCGTCCGACTCTTTTCTCTACTGAGATTCTGTGTGAAATATGAT 80  
DB |||||  
DB 1 TGGTTCCTCGCGTCCGACTCTTTTCTCTACTGAGATTCTGTGTGAAATATGAT 60  
QY 81 TGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTGAA 140  
DB |||||  
DB 61 TGGCGAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTGAA 120  
QY 141 GTGATTGGCGCTATCGGCCCGAGCAGTTCAGTGATGAAGTGAACACCACTGAA 200  
DB |||||  
DB 121 ATGATTGGCGCTATCGGCCCGAGCAGTTCAGTGATGAAGTGAACACCACTGAA 180  
QY 201 GAAGGGGAACCAAGCAACTCAAGCTCAGGATCCTGAGTGTCTCAGGAGGAGGATGAG 260  
DB |||||  
DB 181 GAAGGGGAACCAAGCAACTCAAGCTCAGGATCCTGAGTGTCTCAGGAGGAGGATGAG 240  
QY 261 GGAGCATCTGAGGTCAAGGCCGAGCTGAAGCTGATAGCCAGGAACAGGTCACCCA 320  
DB |||||  
DB 241 GGAGCATCTGAGGTCAAGGCCGAGCTGAAGCTGATAGCCAGGAACAGGTCACCCA 300  
QY 321 CAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGACCCGCCAATCCA 380  
DB |||||  
DB 301 CAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGATGACCCGCCAATCCA 360  
QY 381 CAGGAGGTGAACCGCTCAAGAGAGGTGAAGAGCAATCACAGTGTAAAGAGGACCT 440  
DB |||||  
DB 361 CAGGAGGTGAACCGCTCAAGAGAGGTGAAGAGCAATCACAGTGTAAAGAGGACCT 420

QY 441 TGAATGATGAGGCTCTCTATGTTGGAAATTTGTTCAATTAATAATTTCTCCCAATAAG 500  
 DDb 421 TGAATGATGAGGCTCTCTATGTTGGAAATTTGTTCAATTAATAATTTCTCCCAATAAG 480  
 QY 501 CTTTACAGCCTTCTGCAAGAAAAA 532  
 DDb 481 CTTTACAGCCTTCTGCAAGAAAAA 512

## RESULT 7

ADAL5801  
 ID ADAL5801 standard; cDNA; 528 BP.

XX AC  
 ADAL5801;

XX 06-NOV-2003 (first entry)

DE Human GAGE-8 cDNA.

XX Human; GAGE-8; gene; ss; cytolytic T lymphocyte; CTL;  
 KW human leukocyte antigen; HLA; tumour rejection antigen precursor;  
 KW major histocompatibility complex; MHC; cytolytic T cell proliferation;  
 KW chromosome Xp11.2-p11.4.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 73..423

XX /\*tag= a

XX /product= "Human GAGE-8"

XX /transl\_except= (pos:244..246, aa:Gln)

XX /transl\_except= (pos:400..402, aa:Lys)

XX US6509172-B1.

XX 21-JAN-2003.

XX 30-SEP-1998; 98US-00163748.

XX 30-SEP-1998; 98US-00163748.

XX (LUDW-) LUDWIG INST CANCER RES.

XX De Backer O, Van Den Eynde B, Boon-Falleur T;

XX WPI; 2003-401119/38.

XX P-PSDB; ADAL5778.

XX New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor  
 rejection antigen precursors, which complex to major histocompatibility  
 complex molecules to facilitate the proliferation of cytolytic T cells.

XX Claim 1; Col 7-10; 15pp; English.

XX The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the  
 CC nucleic acid molecules encoding them. The invention also relates to an  
 CC expression vector comprising an isolated nucleic acid molecule of the  
 CC invention operably linked to a promoter, a recombinant cell comprising  
 CC the isolated nucleic acid molecule or the expression vector and an  
 CC expression kit useful in generating cytolytic T lymphocytes (CTLs) or  
 CC determining if CTLs are present in a sample comprising the isolated  
 CC nucleic acid molecule and the isolated nucleic acid that encodes a human  
 CC leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid  
 CC molecules encode tumour rejection antigen precursors, which complex to  
 CC major histocompatibility complex (MHC) molecules to facilitate the  
 CC proliferation of cytolytic T cells. This sequence represents cDNA  
 CC encoding the human GAGE-8 polypeptide of the invention. The gene resides  
 CC on chromosome Xp11.2-p11.4.

SQ Sequence 528 BP; 158 A; 112 C; 151 G; 107 T; 0 U; 0 Other;

Query Match 94.8%; Score 504.4; DB 7; Length 528;

Best Local Similarity 98.3%; Pred. No. 5.5e-136;  
 Matches 521; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 3 CTGTGAGGCAAGTGTCTGTGTGGTTCCTGCGCCCTCGGACTCTTTTCTCTCTAGATCA 62  
 DDb 1 CTGTGAGGCAAGTGTCTGTGTGGTTCCTGCGCCCTCGGACTCTTTTCTCTCTAGATCA 60  
 QY 63 TCTGTGTGAAATATGAGTTGGCGGAGGAAGATGACCTATTATTGGCCCTAGACCAAGGCG 122  
 DDb 61 TCTGTGTGAAATATGAGTTGGCGGAGGAAGATGACCTATTATTGGCCCTAGACCAAGGCG 117  
 QY 123 TATGTACAGCCTCTCTGAAAGTATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTG 182  
 DDb 118 TACGTAGAGCCTCTCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTG 177  
 QY 183 GAACCCAGCAACCTCTGAAAGGGAACCAAGCACTCAACGTGAGGATCTCTGAGCTGCT 242  
 DDb 178 GAACCCAGCAACCTCTGAAAGGGAACCAAGCACTCAACGTGAGGATCTCTGAGCTGCT 237  
 QY 243 CAGGAGGAGGAGATGAGGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATAGC 302  
 DDb 238 CAGGAGGAGGAGATGAGGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATAGC 297  
 QY 303 CAGGAAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGCAGGAG 362  
 DDb 298 CAGGAAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGCAGGAG 357  
 QY 363 ATGGACCCGCCAAATCCAGAGGAGGTGAACCCCTGAAGAGGTGAAGAGCAATCAAG 422  
 DDb 358 ATGGACCCGCCAAATCCAGAGGAGGTGAACCCCTGAAGAGGTGAAGAGCAATCAAG 417  
 QY 423 TGTATAAAGAGGACGCTTGAATGATGACAGGCTGCTCTCTATGTTGAAATTTGTTCAAT 482  
 DDb 418 TGTATAAAGAGGACGCTTGAATGATGACAGGCTGCTCTCTATGTTGAAATTTGTTCAAT 477  
 QY 483 AAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 532  
 DDb 478 AAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 527

## RESULT 8

ABZ20463

ID ABZ20463 standard; cDNA; 530 BP.

XX AC ABZ20463;

XX DT 23-JAN-2003 (first entry)

XX GAGE-2 full length cDNA sequence SEQ ID NO:2890.

XX Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
 KW immune response; virology; immunology; microbiology; molecular biology;  
 KW recombinant DNA technology; gene; ss.

XX Homo sapiens.

XX WO200278516-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US010421.

XX PR 30-MAR-2001; 2001US-0280255P.

XX PR 28-AUG-2001; 2001US-0315563P.

XX PR 09-JAN-2002; 2002US-0347313P.

XX PA (CORI-) CORIXA CORP.

XX XX Wang T, Wang S, Bangur CS, Gaiger A;

XX WPI; 2003-058387/05.

XX DR P-PSDB; ABP54447.

XX XX

PT New immunogenic polynucleotides or polypeptides useful for diagnosing,  
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
PT virology, immunology, microbiology, molecular biology and recombinant DNA  
PT techniques.

XX Claim 1; SEQ ID NO 2890; 207pp; English.

XX ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
CC invention. (I) and (II) have cytostatic activity and can be used in gene  
CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques. N.B. The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 530 BP; 152 A; 116 C; 155 G; 107 T; 0 U; 0 Other;

Query Match 93.4%; Score 496.8; DB 7; Length 530;

Best Local Similarity 98.1%; Pred. No. 8.9e-134;

Matches 514; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

QY 1 AGCTGTGAGGAGTGTGTGTGTTCTCGCTCGGACTCTTTTCTCTACTGAGATT 60

Db |||||

10 AGCTGTGAGGAGTGTGTGTGTTCTCGCTCGGACTCTTTTCTCTACTGAGATT 69

QY 61 CATCTGTGTGAATATGATTCGCGAGGAAGATCGACCTATTATGGCCCTAGACCAAGGC 120

Db |||||

70 CATCTGTGTGAATATGATTCGCGAGGAAGATCGACCTATTATGGCCCTAGACCAAGGC 126

QY 121 GGTATGTACAGCTCTGTAAGTGTATGGCCCTATGCGGCCGAGAGTTCAGTGTGAAG 180

Db |||||

127 GCTACGTAGAGCTCTCTGAAATGATTGGGCCCTATGCGGCCGAGAGTTCAGTGTGAAG 186

QY 181 TGGAAACAGCAACCTCGAAGAGGGGACCAAGCACTCAACGTGAGGATCTCGAGCTG 240

Db |||||

187 TGGAAACAGCAACCTCGAAGAGGGGACCAAGCACTCAACGTGAGGATCTCGAGCTG 246

QY 241 CTCAGGAGGAGGAGGAGGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATA 300

Db |||||

247 CTCAGGAGGAGGAGGAGGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAAGCTGATA 306

QY 301 GCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGGCGAG 360

Db |||||

307 GCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGGCGAG 366

QY 361 AGATGACCCGCAATCCAGAGGAGGTGAACCCCTGAGAGGCTGAAGAGCAATCAC 420

Db |||||

367 AGATGACCCGCAATCCAGAGGAGGTGAACCCCTGAGAGGCTGAAGAGCAATCAC 426

QY 421 AGTGTATAAAGAGGACGCTTGAATATGATGACGAGGCTGCTCTATGTTGAAATTTGTTCA 480

Db |||||

427 AGTGTATAAAGAGGACGCTTGAATATGATGACGAGGCTGCTCTATGTTGAAATTTGTTCA 486

QY 481 TTAAATTTCTCCATATAAGCTTTACAGCTTCTGCAAGAAAA 524

Db |||||

487 TTAAATTTCTCCATATAAGCTTTACAGCTTCTGCAAGAAAA 530

RESULT 9

AAC02129

ID AAC02129 standard; cDNA; 430 BP.

XX AC

XX AAC02129;

XX DT

06-OCT-2000 (first entry)

XX DE

XX Human secreted protein 5' EST, SEQ ID NO: 2127.

XX KW

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-00200610.

XX PR 26-FEB-1999; 99US-0122487P.

XX PA (GEST ) GENSET.

XX PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX DR P-PSDB; MAG02123.

XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for

obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for

diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 2127; 71pp + Sequence Listing; English.

CC The present sequence is one of a large number of 5' ESTs derived from

MRNAs encoding secreted proteins. An ORF has been identified within the

sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs

derived from 30 different tissues. EST sequences usually correspond

mainly to the 3' untranslated region (UTR) of the mRNA because they are

often obtained from oligo-dT primed cDNA libraries. Such ESTs are not

well suited for isolating cDNA sequences derived from the 5' ends of

MRNAs and even in those cases where longer cDNA sequences have been

obtained, the full 5' UTR is rarely included. 5' ESTs are derived from

MRNAs with intact 5' ends and can therefore be used to obtain full length

cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,

gene therapy and chromosome mapping procedures. They are used to obtain

upstream regulatory sequences and to design expression and secretion

vectors

XX SQ

Sequence 430 BP; 101 A; 102 C; 134 G; 85 T; 0 U; 8 Other;

Query Match 65.9%; Score 350.8; DB 3; Length 430;

Best Local Similarity 97.6%; Pred. No. 1.9e-91;

Matches 360; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 1 AGCTGTGAGGAGTGTGTGTGTTCTCGCTCGGACTCTTTTCTCTACTGAGATT 60

Db |||||

63 AGCTGTGAGGAGTGTGTGTGTTCTCGCTCGGACTCTTTTCTCTACTGAGATT 122

QY 61 CATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTTGGCTAGACCAAGGC 120

Db |||||

123 CATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTTGGCTAGACCAAGGC 181

QY 121 GCTATGTACAGCTCTGAAAGTGTGGCCCTATGCGGCCGAGAGTTCAGTGTGAAG 180

Db |||||

182 GCTATGTACAGCTCTGAAAGTGTGGCCCTATGCGGCCGAGAGTTCAGTGTGAAG 241

QY 181 TGGAAACAGCAACCTCGAAGAGGGGAAACAGCACTCAACGTGAGGATCTCGAGCTG 240

Db |||||

242 TGGAAACAGCAACCTCGAAGAGGGGAAACAGCACTCAACGTGAGGATCTCGAGCTG 301

QY 241 CTCAGGAGGAGGAGGATGAGGAGCATCTGCAAGTCAAGGGCCGAGGCTGAAGCTGATA 300

Db |||||

302 CTCAGGAGGAGGATGAGGAGCATCTGCAAGTCAAGGGCCGAGGCTGAAGCTGATA 361

QY 301 GCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGGCGAG 360

Db |||||

362 GCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGGCGAG 421

QY 361 AGATGGACC 369

Db |||||

422 AGATGGACC 430



CC	disease and tumours (e.g. glioma). The present sequence is one of the
CC	1046 novel cancer cell markers
xx	
SQ	Sequence 365 BP; 63 A; 86 G; 66 C; 150 T; 0 U; 0 Other;
	Query Match 56.8%; Score 302.4; DB 4; Length 365;
	Best Local Similarity 96.68; Pred. No. 2e-77;
	Matches 309; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY	213 GCAACTCAAAGTTCAGGATCTGTGACGTGCTCAGAGGGAGGAGGATGAGGGAGCATCTGCA 272
Db	365 GCAACTCAAAGTTCAGGATCTGTGACGTGCTCAGAGGGAAAGGATAAGGGAGCATCTGCA 306
QY	273 GGTCAAGGGCGCGAAGCTGAAGCTGATAGCCAGGAACAGGGTGACCCACAGACTGGGTGT 332
Db	305 GGTCAAGGGCGCGAAGCTGAAGCTGATAGCCAGGAACAGGGTGACCCCGAGACTGGGTGT 246
QY	333 GAGTGTCAAGATGTCTCTGATGGGCAGAGATGACCCTGCCCAATTCAGAGGAGGTGAAA 392
Db	245 GAGTGTGAATAATGTCTCTGATGGGCAGGAATGGACCCGCCCAATCCAAAGGAGGTGAAA 186
QY	393 ACGCTTGAAGAAGTGTAAAAACAATCACAGTGTTTAAAAAGAGGCACCTTGCAATGATGCA 452
Db	185 ACGCTTGAAGAAGTGTAAAAAGCAATCTCAGTGTTTAAAAAAGGCACGTTGAATGATGCA 126
QY	453 GGCTGCTCCTCATGTTGGAATTTGTTCAATTAAAAATCTCCCAATAAAGCTTTACAGCCTT 512
Db	125 GGCTGCTCCTCATGTTGGAATTTGTTCAATTAAAAATCTCCCAATAAAGCTTTACAGCCTT 66
QY	513 CTGCAAAAGAAAAAAAAAAAA 532
Db	65 CTAAAAAAAAAAAAAAAAAAAA 46

RESULT 12	
ABZ19551/c	
ID ABZ19551 standard; cDNA; 277 BP.	
XX	
XX	
AC AC	
ABZ19551;	
XX	
XX	
DT 23-JAN-2003 (first entry)	
XX	
DE Group III cDNA cancer related clone SEQ ID NO:1977.	
XX	
XX	
KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;	
KW immune response; virology; immunology; microbiology; molecular biology;	
KW recombinant DNA technology; gene; ss.	
XX	
XX	
OS Homo sapiens.	
XX	
XX	
PN WO200278516-A2.	
XX	
XX	
PD 10-OCT-2002.	
XX	
XX	
PF 28-MAR-2002; 2002WO-US010421.	
XX	
XX	
PR 30-MAR-2001; 2001US-0280255P.	
PR 28-AUG-2001; 2001US-0315563P.	
PR 09-JAN-2002; 2002US-0347313P.	
XX	
XX	
PA (CORI-) CORIXA CORP.	
XX	
XX	
P1 Wang T, Wang S, Bangur CS, Gaiger A;	
XX	
XX	
DR WPI; 2003-058387/05.	
XX	
XX	
PT New immunogenic polynucleotides or polypeptides useful for diagnosing,	
PT Preventing and treating cancer expressing CT or CP mRNA antigens, and in	
PT virology, immunology, microbiology, molecular biology and recombinant DNA	
PT techniques.	
XX	
XX	
PS Claim 1; SEQ ID NO 1977; 207pp; English.	
XX	

CC	ABQ17575	to	ABQ20506	represent	isolated	polynucleotide	(I)	sequences,	and
CC	ABP5446	to	ABP5472	represent	protein	(II)	sequences,	from	the
CC	invention.	(I)	and	(II)	have	cytostatic	activity	and	can
CC	therapy	and	vaccines.	(I),	(II),	antibodies	and	compositions	from
CC	present	invention	are	useful	for	diagnosing,	preventing	and	treating
CC	cancer,	which	expresses	Ct	or	CP	mRNA	antigens.	They
CC	are	useful	for	stimulating	immune	response.	They	can	also
CC	be	useful	in	immunology,	microbiology,	molecular	biology	and	recombinant
CC	techniques.	N.B.	The	sequence	data	for	this	patent	did
CC	not	form	part	of	the	printed	specification,	but	was
CC	obtained	in	electronic	format	directly	from	WIPO	at	ftp.wipo.int/pub/published_pct_sequences
CC	XX								
CC	Sequence	277	BP;	62	A;	79	C;	73	G;
CC	63	T;	0	U;	0	Other;			
CC	Query	March	44.5%;	Score	237;	DB	7;	Length	277;
CC	Best	Local	Similarity	100.0%;	Prod.	No.	1.6e-58;		
CC	Matches	237;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
CC	0;								
QY	1	AGCTGTGAGGCAGTGTGTGGTTCCTGCGCTCGGACCTCTTTTCTCTACTGAGATT	60						
Db	237	AGCTGTGAGGCAGTGTGTGGTTCCTGCGCTCGGACCTCTTTTCTCTACTGAGATT	178						
QY	61	CATCTGTGTGAAATATGAGTTGGCGAGGAGATCGACTATATTGGCCTAGACCAAGGC	120						
Db	177	CATCTGTGTGAAATATGAGTTGGCGAGGAGATCGACTATATTGGCCTAGACCAAGGC	118						
QY	121	GCTATGTACAGCCCTCTTGAAGTGAATGGGCCCTATGGGCCCGCAGCAGTTCAAGTCATGAAG	180						
Db	117	GCTATGTACAGCCCTCTTGAAGTGAATGGGCCCTATGGGCCCGCAGCAGTTCAAGTCATGAAG	58						
QY	181	TGGAAACAGCAACACTCTGAAGAAAGGGGAAACAGCAACTCAACGTACAGATCCTGCAG	237						
Db	57	TGGAAACAGCAACACTCTGAAGAAAGGGGAAACAGCAACTCAACGTACAGATCCTGCAG	1						

RESULT 13	
ABZ19955/c	
ID	ABZ19955 standard; cDNA; 257 BP.
XX	
AC	ABZ19955;
XX	
DT	23-JAN-2003 (first entry)
XX	
DE	Group III cDNA cancer related clone SEQ ID NO:2381.
XX	
KW	Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
KW	immune response; virology; immunology; microbiology; molecular biology;
KW	recombinant DNA technology; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200278516-A2.
XX	
PD	10-OCT-2002.
XX	
PF	28-MAR-2002; 2002WO-US010421.
XX	
PR	30-MAR-2001; 2001US-0280255P.
PR	28-AUG-2001; 2001US-0315563P.
PR	09-JAN-2002; 2002US-0347313P.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Wang T, Wang S, Bangur CS, Gaiger A;
XX	
DR	WPI; 2003-058387/05.
XX	
PT	New immunogenic polynucleotides or polypeptides useful for diagnosing,
PT	preventing and treating cancer expressing CT or CP mRNA antigens, and
PT	virology, immunology, microbiology, molecular biology and recombinant
PT	techniques.
XX	
PS	Claim 1; SEQ ID NO 2381; 207pp; English.

XX ABO17575 to ABO20506 represent isolated polynucleotide (I) sequences, and  
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
CC invention. (I) and (II) have cytosstatic activity and can be used in gene  
CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques. N.B. The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 257 BP; 57 A; 74 C; 62 G; 64 T; 0 U; 0 Other;

Query Match 44.2%; Score 235.4; DB 7; Length 257;  
Best Local Similarity 99.6%; Pred. No. 4.6e-59;  
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGCTGTGAGGCGAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60  
Db 237 AGCTGTGAGGCGAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 178  
QY 61 CATCTGTGAAATATAGATTGGCGAGGAAGATCGACCTATTATTGCGCTTAGACCAAGGC 120  
Db 177 CATCTGTGAAATATAGATTGGCGAGGAAGATCGACCTATTATTGCGCTTAGACCAAGGC 118  
QY 121 GCTATGTACAGCCTCCTGAGTGATTGGGCTTATGCGGCCCGAGCAGTTCAGTGATGAAG 180  
Db 117 GCTATGTACAGCCTCCTGAGTGATTGGGCTTATGCGGCCCGAGCAGTTCAGTGATGAAG 58  
QY 181 TGGAAACAGCAACACCTGAGAGAGGGGAACAGCAACTCAACGTCAGGATCCTGCAG 237  
Db 57 TGGAAACAGCAACACCTGAGAGAGGGGAACAGCAACTCAACGTCAGGATCCTGCAG 1

RESULT 14  
ABZ19755  
ID ABZ19755 standard; cDNA; 264 BP.  
XX  
AC ABZ19755;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE Group III cDNA cancer related clone SEQ ID NO:2181.  
XX  
KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
KW immune response; virology; immunology; microbiology; molecular biology;  
KW recombinant DNA technology; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200278516-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US010421.  
XX  
PR 30-MAR-2001; 2001US-0280255P.  
PR 28-AUG-2001; 2001US-0315563P.  
PR 09-JAN-2002; 2002US-0347313P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
XX Wang T, Wang S, Bangur CS, Gaiger A;  
XX  
XX WPI; 2003-058387/05.

New immunogenic polynucleotides or polypeptides useful for diagnosing,  
preventing and treating cancer expressing CT or CP mRNA antigens, and in  
virology, immunology, microbiology, molecular biology and recombinant DNA  
techniques.

PS Claim 1; SEQ ID NO 2181; 207pp; English.  
XX  
XX ABO17575 to ABO20506 represent isolated polynucleotide (I) sequences, and  
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
CC invention. (I) and (II) have cytosstatic activity and can be used in gene  
CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques. N.B. The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 264 BP; 64 A; 66 C; 75 G; 59 T; 0 U; 0 Other;

Query Match 44.2%; Score 235.4; DB 7; Length 264;  
Best Local Similarity 99.8%; Pred. No. 4.7e-58;  
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGCTGTGAGGCGAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60  
Db 28 AGCTGTGAGGCGAGTGTGTGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 87  
QY 61 CATCTGTGAAATATAGATTGGCGAGGAAGATCGACCTATTATTGCGCTTAGACCAAGGC 120  
Db 88 CATCTGTGAAATATAGATTGGCGAGGAAGATCGACCTATTATTGCGCTTAGACCAAGGC 147  
QY 121 GCTATGTACAGCCTCCTGAGTGATTGGGCTTATGCGGCCCGAGCAGTTCAGTGATGAAG 180  
Db 148 GCTATGTACAGCCTCCTGAGTGATTGGGCTTATGCGGCCCGAGCAGTTCAGTGATGAAG 207  
QY 181 TGGAAACAGCAACACCTGAGAGAGGGGAACAGCAACTCAACGTCAGGATCCTGCAG 237  
Db 208 TGGAAACAGCAACACCTGAGAGAGGGGAACAGCAACTCAACGTCAGGATCCTGCAG 264

RESULT 15  
ABZ20497  
ID ABZ20497 standard; cDNA; 229 BP.  
XX  
AC ABZ20497;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE TPS1 subtraction library cDNA clone SEQ ID NO:2950.  
XX  
KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
KW immune response; virology; immunology; microbiology; molecular biology;  
KW recombinant DNA technology; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200278516-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US010421.  
XX  
PR 30-MAR-2001; 2001US-0280255P.  
PR 28-AUG-2001; 2001US-0315563P.  
PR 09-JAN-2002; 2002US-0347313P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
XX Wang T, Wang S, Bangur CS, Gaiger A;  
XX  
XX WPI; 2003-058387/05.

New immunogenic polynucleotides or polypeptides useful for diagnosing,  
preventing and treating cancer expressing CT or CP mRNA antigens, and in  
virology, immunology, microbiology, molecular biology and recombinant DNA  
techniques.

```
XX Claim 1; SEQ ID NO 2950; 207pp; English.
PS
XX
CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
CC ABP5446 to ABP54472 represent protein (II) sequences, from the present
CC invention. (I) and (II) have cytosolic activity and can be used in gene
CC therapy and vaccines. (I), (II), antibodies and compositions from the
CC present invention are useful for diagnosing, preventing and treating
CC cancer, which expresses CT or CP mRNA antigens. They are useful for
CC stimulating immune response. They can also be useful in virology,
CC immunology, microbiology, molecular biology and recombinant DNA
CC techniques. N.B. The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 229 BP; 56 A; 55 C; 64 G; 54 T; 0 U; 0 Other;

Query Match          42.7%; Score 227.4; DB 7; Length 229;
Best Local Similarity 99.6%; Pred. No. 9.2e-56;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGCAGTGTGTGTGTTCTCTGCGGTCGGACCTCTTTCTCTACTGAGATTCATCTGTG 68
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1 GGCAGTGTGTGTGTTCTCTGCGGTCGGACCTCTTTCTCTACTGAGATTCATCTGTG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 69 TGAATATGAGTTGGCGAGGAGATCCACTATTATTGGCTAGACCAAGCGCTATGTA 128
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 TGAATATGAGTTGGCGAGGAGATCCACTATTATTGGCTAGACCAAGCGCTATGTA 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 129 CAGCTTCTGAGTGTGTTGGGCTATGCGGCGGAGCAGTTCAAGTGAAGTGAACCA 188
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 CAGCTTCTGAGTGTGTTGGGCTATGCGGCGGAGCAGTTCAAGTGAAGTGAACCA 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 189 GCAACACCTGAGAGAGGGGAACAGCACTCAACGTCAGATCCTGCAG 237
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 GCAACACCTGAGAGAGGGGAACAGCACTCAACGTCAGATCCTGCAG 229
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: August 6, 2004, 19:34:18
Job time : 335 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 19:34:25 ; Search time 374 Seconds  
(without alignments)  
3521.250 Million cell updates/sec

Title: US-09-782-745-17

Perfect score: 532

Sequence: 1 AGCTGTGAGGCGAGTGTGTG.....CTCCAAAGAAAAA 532

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4761877 seqs, 1237732561 residues

Total number of hits satisfying chosen parameters: 8521116

Minimum DB seq length: 0

Maximum DB seq length: 532

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents NA New:

- 1: /cgn2\_6/prodata/1/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/prodata/1/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/prodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/prodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/prodata/1/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/prodata/1/pna/US10\_NEW\_COMB.seq.\*
- 7: /cgn2\_6/prodata/1/pna/US10\_NEW\_COMB.seq.\*
- 8: /cgn2\_6/prodata/1/pna/US10\_NEW\_COMB.seq.\*
- 9: /cgn2\_6/prodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517.4	97.3	528	7	US-10-782-413-16
2	350.8	65.9	430	7	US-10-793-479-2127
3	208.4	39.2	520	8	US-10-473-603-38
4	140	26.3	528	8	US-10-473-603-20
5	137.8	25.9	336	7	US-10-821-234-695
6	133.2	25.0	475	5	US-09-970-607-3
7	133.2	25.0	475	5	US-10-453-372-485
8	128.6	24.2	336	7	US-10-821-234-590
9	118.8	22.3	501	7	US-10-453-372-475
10	118	22.2	448	5	US-09-970-607-44
11	111.6	21.0	448	5	US-09-970-607-43
12	101.6	19.1	515	5	US-09-570-737A-472
13	99.8	18.8	374	7	US-10-453-372-477
14	97.4	18.3	337	7	US-10-453-372-479
15	96.4	18.1	344	7	US-10-453-372-487
16	94.8	17.8	343	7	US-10-453-372-483
17	94.8	17.8	343	7	US-10-453-372-481
18	86.4	16.2	348	5	US-09-970-607-109
19	85.4	16.1	336	7	US-10-453-372-473
20	85.2	16.0	499	1	PCT-US02-22858A-684
21	82.8	15.6	458	7	US-10-453-372-469
22	81.2	15.3	458	5	US-09-970-607-1
23	81.2	15.3	458	7	US-10-453-372-471
24	80.8	15.2	309	7	US-10-821-234-605
					Sequence 16, Appl
					Sequence 2127, Ap
					Sequence 38, Appl
					Sequence 20, Appl
					Sequence 695, App
					Sequence 3, Appli
					Sequence 485, App
					Sequence 590, App
					Sequence 475, App
					Sequence 44, Appl
					Sequence 43, Appl
					Sequence 472, App
					Sequence 477, App
					Sequence 479, App
					Sequence 487, App
					Sequence 483, App
					Sequence 481, App
					Sequence 109, App
					Sequence 473, App
					Sequence 684, App
					Sequence 469, App
					Sequence 1, Appli
					Sequence 471, App
					Sequence 605, App

25	78.6	14.8	334	8	US-10-473-603-46	Sequence 46, Appl
26	57	10.7	69	7	US-10-834-268-3287	Sequence 3287, Ap
27	53	10.0	157	7	US-10-793-479-19668	Sequence 19668, A
c	51	9.6	51	8	US-10-865-478-612	Sequence 612, App
29	49.4	9.3	51	8	US-10-865-478-421	Sequence 421, App
30	49.4	9.3	51	8	US-10-865-478-613	Sequence 613, App
31	48.8	9.2	110	5	US-09-970-607-31	Sequence 31, Appl
32	48.2	9.1	122	5	US-09-970-607-36	Sequence 36, Appl
33	45.6	8.6	110	5	US-09-970-607-32	Sequence 32, Appl
34	43.6	8.2	114	5	US-09-970-607-140	Sequence 140, App
35	41.6	7.8	472	7	US-10-674-124A-5858	Sequence 5858, Ap
36	40.2	7.6	119	5	US-09-970-607-33	Sequence 33, Appl
37	39.6	7.4	415	6	US-10-425-115-51014	Sequence 51014, A
38	39	7.3	395	1	PCT-US04-07668-45	Sequence 45, Appl
39	38.6	7.3	119	5	US-09-970-607-34	Sequence 34, Appl
40	36.6	6.9	387	7	US-10-674-124A-15877	Sequence 15877, A
c	41	36	493	6	US-10-501-933-1267	Sequence 1267, Ap
42	36	6.8	493	9	US-60-554-981-523	Sequence 523, App
c	43	36	493	9	US-60-559-949-207	Sequence 207, App
44	35.4	6.7	356	5	US-09-404-520B-27194	Sequence 27194, A
c	45	35.2	498	6	US-10-425-115-149178	Sequence 149178, A

#### ALIGNMENTS

RESULT 1  
US-10-782-413-16  
; Sequence 16, Application US/10782413  
; GENERAL INFORMATION:  
; APPLICANT: Ortho-Clinical Diagnostics, Inc.  
; APPLICANT: Wang, Yixin  
; TITLE OF INVENTION: Colorectal Cancer Prognostics  
; FILE REFERENCE: VDX-5002 CIP  
; CURRENT APPLICATION NUMBER: US/10/782,413  
; CURRENT FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: 10/651,237  
; PRIOR FILING DATE: 2003-08-28  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 528  
; TYPE: DNA  
; ORGANISM: human  
US-10-782-413-16

Query Match		97.3%	Score 517.4;	DB 7;	Length 528;
Best Local Similarity		99.8%	Pred. No. 1.7e-149;		
Matches 518;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	AGCTGTGAGGCGAGTGTGTGTCTCTCCGTCGGACTCTTTTCTCTACTGAGATT	60		
Db	9	AGCTGTGAGGCGAGTGTGTGTCTCTCTCCGTCGGACTCTTTTCTCTACTGAGATT	68		
QY	61	CATCTGTGGAATATGATTCGGCAGGAGATGACCTATTATGGCCTAGACOMAGGC	120		
Db	69	CATCTGTGGAATATGATTCGGCAGGAGATGACCTATTATTTGGCCTAGACCAAGGC	128		
QY	121	GCTATGTACAGCTCTCTGAAGTATTGGCCCTATGCGCCCGCAGCAGTTTCAGTGATGAG	180		
Db	129	GCTATGTACAGCTCTCTGAATATTGGCCCTATGCGCCCGCAGCAGTTTCAGTGATGAG	188		
QY	181	TGGAAACAGAACACTCTGAAGAAGGGGAAACCAAGCAACTCAAGTCAGGATCTTCAGCTG	240		
Db	189	TGGAAACAGAACACTCTGAAGAAGGGGAAACCAAGCAACTCAAGTCAGGATCTTCAGCTG	248		
QY	241	CTCAGAGGAGAGATGAGGAGCATCTGAGGTCAAGGCCGGAAGCCTGAGCTGATA	300		
Db	249	CTCAGAGGAGAGATGAGGAGCATCTGAGGTCAAGGCCGGAAGCCTGAGCTGATA	308		
QY	301	GCCAGGAACAGGCTCACCCACAGCTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGG	360		
Db	309	GCCAGGAACAGGCTCACCCACAGCTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGG	368		

QY 361 AGATGACCCGCAATCCAGAGAGTGAAGCGCTGAAGAGTGAAGCAATCAC 420  
Db 369 AGATGACCCGCAATCCAGAGAGTGAAGCGCTGAAGAGTGAAGCAATCAC 428  
QY 421 AGTGTAAAGAGGACGTTGAAATGATGAGGCTGCTCTATGTTGGAATTTGTCA 480  
Db 429 AGTGTAAAGAGGACGTTGAAATGATGAGGCTGCTCTATGTTGGAATTTGTCA 488  
QY 481 TTAATAATCCCAATAAAGCTTTACAGCCTTCTGCAAA 519  
Db 489 TTAATAATCCCAATAAAGCTTTACAGCCTTCTGCAAA 527

RESULT 2  
US-10-793-479-2127  
; Sequence 2127, Application US/10793479  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/10/793,479  
; CURRENT FILING DATE: 2004-03-03  
; PRIOR APPLICATION NUMBER: US/09/513,999  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 2127  
; LENGTH: 430  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 202..429  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 31  
; OTHER INFORMATION: n=a, g, c or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 32  
; OTHER INFORMATION: k=g or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 164  
; OTHER INFORMATION: n=a, g, c or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 166  
; OTHER INFORMATION: y=c or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 180  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 283  
; OTHER INFORMATION: y=c or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 307  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 429  
; OTHER INFORMATION: m=a or c  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 28

; OTHER INFORMATION: Xaa=Cys or Arg  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 36  
; OTHER INFORMATION: Xaa=Glu or Lys  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 76  
; OTHER INFORMATION: Xaa=Asp or Glu  
US-10-793-479-2127  
Query Match 65.9%; Score 350.8; DB 7; Length 430;  
Best Local Similarity 97.6%; Pred. No. 4.9e-98;  
Matches 360; Conservative 5; Mismatches 3; Indels 1; Gaps 1;  
QY 1 AGCTGTGAGGAGTGTGTGTTCTGCGCTCCGACTCTTTTCTCTACTGAGATT 60  
Db 63 AGCTGTGAGGAGTGTGTGTTCTGCGCTCCGACTCTTTTCTCTACTGAGATT 122  
QY 61 CATCTGTGAAATATATGATTGGCGAGGAAGATCGACTATATTGGCCCTAGACCAAGGC 120  
Db 123 CATCTGTGAAATATATGATTGGCGAGGAAGATCGACTATNA-YGGCCTAGACCAAGRC 181  
QY 121 GCTATGTACAGCTCTCTCTGAAAGTGTGGGCTATGCGGCCGAGCAGTTCAGTGAAG 180  
Db 182 GCTATGTACAGCTCTCTCTGAAATGATTGGGCTATGCGGCCGAGCAGTTCAGTGAAG 241  
QY 181 TGGAAACAGCAACACCTGGAAGAGGGGAACCCAGCAACTCAACGTGAGGATCCTGCAGCTG 240  
Db 242 TGGAAACAGCAACACCTGGAAGAGGGGAACCCAGCAACTCAAYGTGAGGATCCTGCAGCTG 301  
QY 241 CTCAGGAGGAGAGGATGAGGAGCATCTGCAGTCAAGGCCGAGGCTGAAGCTGATA 300  
Db 302 CTCAGGAGGAGAGGATGAGGAGCATCTGCAGTCAAGGCCGAGGCTGAAGCTGATA 361  
QY 301 GCCAGGAACAGGCTCACCACAGACTGGTGTGATGTGAAGATGCTCTGATGGCAGG 360  
Db 362 GCCAGGAACAGGCTCACCACAGACTGGTGTGATGTGAAGATGCTCTGATGGCAGG 421  
QY 361 AGATGGACC 369  
Db 422 AGATGGACC 430  
RESULT 3  
US-10-473-603-38  
; Sequence 38, Application US/10473603  
; GENERAL INFORMATION:  
; APPLICANT: OLD, Lloyd  
; APPLICANT: SCANLAN, Matthew  
; APPLICANT: CHEN, Yao-Tseng  
; TITLE OF INVENTION: CANCER-TESTIS ANTIGENS  
; FILE REFERENCE: L0461.70155US00  
; CURRENT APPLICATION NUMBER: US/10/473,603  
; CURRENT FILING DATE: 2003-09-30  
; PRIOR APPLICATION NUMBER: PCT/US02/09808  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: 10/054,683  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/280,718  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/285,154  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/327,432  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 38  
; TYPE: DNA  
; LENGTH: 520  
; ORGANISM: Homo sapiens  
US-10-473-603-38

[illegible]

Db 100 CCTCAGCAAGAGAACCCACCACTGAAGTCGGATCCTGCACCTGTCAGGAGAGAA 159  
QY 252 GAGGATGAGGAGCATCTGCAGGTCAAGGCCGAAAGCCTGAAGCTGATGATCCAGGAACAG 311  
Db 160 GAAGATCAGGAGTGCAGCTGAGACTCAAGTGCCTGACCTGGAAGCTGATCTCCAGGAGCTG 219  
QY 312 GGTCAACCCACAGACTGGGTGTGAGTGAAGATGGTCTGATGGGACAGAGATGGACCCG 371  
Db 220 TCTCAGTCAAGAGACTGGGGGTGAATGTGGAATGGTCTGATGACCAAGGGAAGATTCGT 279  
QY 372 CCAAAATCCAGAGAGGTGAAAACGCTGGAAGAGGTGAAAAGCAATCACAAGTGTAA 428  
Db 280 CCAAAATCAGACAACTTAAATGCCAGAGAGAGGTGACAGGCACACAGGTTAA 336

## RESULT 6

US-09-970-607-3  
; Sequence 3, Application US/09970607  
; GENERAL INFORMATION:  
; APPLICANT: Malyankar et al.  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-675 CIP2  
; CURRENT APPLICATION NUMBER: US/09/970,607  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 60/182,733  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/182,724  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/183,896  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/184,497  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/224,157  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/184,482  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,744  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/197,083  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/233,405  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 60/236,060  
; PRIOR FILING DATE: 2000-09-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 475  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-970-607-3

Query Match 25.0%; Score 133.2; DB 5; Length 475;  
Best Local Similarity 59.8%; Pred. No. 9.6e-31;  
Matches 286; Conservative 0; Mismatches 173; Indels 19; Gaps 3;

QY 61 CATCTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGC 120  
Db 11 CATGTGTGGAATATGAGTCAGCATGTGAGAACAAAGATCCCAATCCTCAGAAAGAGAA 70  
QY 121 GCTATGTACAGCTCTGAGTGTGGCCCTATCGGCCCGAGCAGTTCAGTGATGAAG 180  
Db 71 ATGACCAAGAGCTTCCCGACGAGTTGGATCTGTGATGTCAGAGGCCACTGAGGA-- 128  
QY 181 TGAACACAGCAACCTGAAAGAGGGGACCAAGCAACTCAACGTGAGGATCCTGAGCTG 240  
Db 129 -----AAAACTCAGAAGAGGAACCAACCAACTGATAATCAGGGTATTGCACCTA 178  
QY 241 CTCAGAGGAGAGGATGAGGAGGATCTGAGGTCAAGGCCGAGCCCTGAGCTGATA 300  
Db 179 GTGGGAGATCGAAAATGAAGGAGCACCTGCCCTTCAAGGCGCTGATGGAAGCTTTTC 238

QY 301 GCAGGAAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCCTGATGGGAGG 360  
Db 239 AACAGGAACCTGGCTCTGCTTACATAGAGATGAGCTGGAGATGCTCTGATGTCAGGG 298  
QY 361 AGTGAACCCCGCCAAATCCAGAGGAGGTGAAACGCTGAGAGAGGTGAAAAGCAATCAC 420  
Db 299 AGGGGATTAATGCCCACTTTTGTGATCTCACTAAAGTGTGGAAGCAGGTGATGCCCAACAT 358  
QY 421 AGTGTAAAAGAGGACCGT-----TGAATGATGAGGCTGCTCCTATGTTGGAATT 474  
Db 359 AGTGTCAAGCAAGACAAATGAAGACTGAAACCCAGAACGTTATTCTTAATCTGGAATT 418  
QY 475 TGTTCAATTAATTTCTCCCAATAAAGCTTTTACAGCCTTCTGCAAGAAAAA 532  
Db 419 TGACTGATAATATCTCTTAATAAGTTTAA-AGTTTTCTGCAAGAAAAA 475

## RESULT 7

US-10-453-372-485  
; Sequence 485, Application US/10453372  
; GENERAL INFORMATION:  
; APPLICANT: Alsbrook, et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-589 A  
; CURRENT APPLICATION NUMBER: US/10/453,372  
; CURRENT FILING DATE: 2003-06-03  
; PRIOR APPLICATION NUMBER: 09/789390  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/185967  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 09/823187  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/195792  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 09/839446  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 60/199476  
; PRIOR FILING DATE: 2000-03-25  
; PRIOR APPLICATION NUMBER: 09/863776  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: 60/208263  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 09/939398  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/227800  
; PRIOR FILING DATE: 2000-08-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1609  
; SOFTWARE: CuraSeqlist version 0.1  
; SEQ ID NO 485  
; LENGTH: 475  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(357)  
US-10-453-372-485

Query Match 25.0%; Score 133.2; DB 7; Length 475;  
Best Local Similarity 59.8%; Pred. No. 9.6e-31;  
Matches 286; Conservative 0; Mismatches 173; Indels 19; Gaps 3;

QY 61 CATCTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGC 120  
Db 11 CATGTGTGGAATATGAGTCAGCATGTGAGAACAAAGATCCCAATCCTCAGAAAGAGAA 70  
QY 121 GCTATGTACAGCTCTGAGTGTGGCCCTATCGGCCCGAGCAGTTCAGTGATGAAG 180  
Db 71 ATGACCAAGAGCTTCCCGACGAGTTGGATCTGTGATGTCAGAGGCCACTGAGGA-- 128  
QY 181 TGAACACCAACACACTGAAAGAGGGGACCAAGCAACTCAACGTGAGGATCCTGAGCTG 240

Db 129 -----AAAACGTCAAGAGAGGAACACCAACTGATAATACAGGGTATTGCACCTA 178  
 Qy 241 CTCAGAGGAGAGGATGAGGAGCATCTGCAGCTCAAGGCCAAGCCTGAAGCTGATA 300  
 Db 179 GTGGGAGATCGAANAATGAAGGACACTGCGCTCAAGGCCCTGACATGAAGCTTTTC 238  
 Qy 301 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTAGTGTGAAGATGGTCTCTGATGGCAGG 360  
 Db 239 AACAGGAACCTGGTCTCTCTTAAGATAGAGGTAGCTGGAGATGGTCTCTGATGCAGG 298  
 Qy 361 AGATGGACCCGCCAATCCAGAGAGGTGAAGAGCCTGAAGAGGTCAAAAGCAATCAC 420  
 Db 299 AGGGATATTGCGCCACTTTTGTCTCACTAAAGTGTGAAGCAGGTGATGCGCAACCAT 358  
 Qy 421 AGTGTAAAGAGGACAGT-----TGAATGATGAGGCTGCTCTCTATGTTGGAATTT 474  
 Db 359 AGGTTTCAAGCAAGACAAATGAAGACTGAACCAAGAACCTTATCTTAATCTGGAATTT 418  
 Qy 475 TGTTCATTAAATCTCCCAATAAAGCTTTTACAGCCTTCTGCAAGAGAAAAA 532  
 Db 419 TGACTGATAATATCTCTTAATAAAGTTTAA-AGTTTCTGCAAGAGAAAAA 475

## RESULT 8

US-10-821-234-590  
 ; Sequence 590, Application US/10821234  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Labat, Ivan  
 ; APPLICANT: Stache-Crain, Birgit  
 ; APPLICANT: Andarmani, Susan  
 ; APPLICANT: Tang, Y. Tom  
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
 ; FILE REFERENCE: 821A  
 ; CURRENT APPLICATION NUMBER: US/10/821,234  
 ; PRIOR FILING DATE: 2004-04-07  
 ; PRIOR APPLICATION NUMBER: US 60/462,047  
 ; NUMBER OF SEQ ID NOS: 1704  
 ; SOFTWARE: pt\_seq\_genes Version 1.0  
 ; SEQ ID NO 590  
 ; LENGTH: 336  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-821-234-590

Query Match 24.2%; Score 128.6; DB 7; Length 336;  
 Best Local Similarity 66.9%; Pred. No. 2.1e-29;  
 Matches 239; Conservative 0; Mismatches 94; Indels 24; Gaps 3;  
 Qy 75 ATGAGTTGCGAGGAGATCGACCTATTATTGGCCTTAGACCAGGCGCTATCTACAGCCT 134  
 Db 1 ATGAGTTGCGAGGAGATCAAC---ATATAGCCTTAGCCAGGAGAGAGTTTACAGCCT 57  
 Qy 135 CTGAGTGTATGGGCTTATGCGGCCGAGCAGTTTCAAGTATGAAGTGAACCAACA 194  
 Db 58 CTTGAGCTGATTTGGGGCTATGCT-----TGAACCCACTGATGAAG 99  
 Qy 195 CTGAAGAGGGGACCAAGCACTCAAGCTCAGATCTCTGAGCTGCTCAGAGGGAGAG 254  
 Db 100 CTTAAGAGAGAAACCAACCACTAAAGTGGAAATCTTACACCTGATCAGAAGAGAA 159  
 Qy 255 GATG---AGGAGCATCTCAGGTCAAGGCCCGAAGCCTGAAGCTGATAGCCAGGAACAG 311  
 Db 160 GATGATCAGGTGTCAGCTGAGATTCAGTGTCTGACCTGGAAGCCGATCTCAGAGCTA 219  
 Qy 312 GGTCAACACAGATGGGTGTGAGTGTGAAGATGCTCTCTGATGGCAGGAGATGACCCG 371  
 Db 220 TGTCAACAAGACTGGGGATGATGTGAAGTGTGTACTGATGTCAAGGGAGATTCTTA 279  
 Qy 372 CCAATCCAGAGGAGGTGAAGCGCTCAAGAGGTGAAGAGCAATCAAGTGTAA 428  
 Db 280 CCAAGCAGAGCATTTTAAATATGCCAAGCAGGTGAAGGGAATATCAGAGTTTAA 336

## RESULT 9

US-10-453-372-475  
 ; Sequence 475, Application US/10453372  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alsobrook, et al.  
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 ; FILE REFERENCE: 21402-589 A  
 ; CURRENT APPLICATION NUMBER: US/10/453,372  
 ; CURRENT FILING DATE: 2003-06-03  
 ; PRIOR APPLICATION NUMBER: 09/789390  
 ; PRIOR FILING DATE: 2001-02-23  
 ; PRIOR APPLICATION NUMBER: 60/185967  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: 09/823187  
 ; PRIOR FILING DATE: 2001-03-29  
 ; PRIOR APPLICATION NUMBER: 60/195792  
 ; PRIOR FILING DATE: 2000-03-10  
 ; PRIOR APPLICATION NUMBER: 09/839446  
 ; PRIOR FILING DATE: 2001-03-19  
 ; PRIOR APPLICATION NUMBER: 60/199476  
 ; PRIOR FILING DATE: 2000-03-25  
 ; PRIOR APPLICATION NUMBER: 09/863776  
 ; PRIOR FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: 60/208263  
 ; PRIOR FILING DATE: 2000-05-31  
 ; PRIOR APPLICATION NUMBER: 09/939398  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: 60/227800  
 ; PRIOR FILING DATE: 2000-08-25  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 1609  
 ; SOFTWARE: CuraSeqList version 0.1  
 ; SEQ ID NO 475  
 ; LENGTH: 501  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (25)..(357)  
 US-10-453-372-475

Query Match 22.3%; Score 118.8; DB 7; Length 501;  
 Best Local Similarity 57.9%; Pred. No. 2.8e-26;  
 Matches 277; Conservative 0; Mismatches 182; Indels 19; Gaps 3;  
 Qy 61 CATCTGTGTGAATATGATGTTGGCCAGGAAGATCAACCTATTATTGGCTAGACCAAGC 120  
 Db 11 CATGTGTGGGAATATGATGAGTGTGTAAGAACCAAGATCCCAATCCTCAGAAAGAGAA 70  
 Qy 121 GCTATGTACAGCCTCTGAAAGTGAATTGGGCTTATCGGCCCGAGCAGTTCAGTGATGAAG 180  
 Db 71 ATGACCAAGAGTCTTCCAGCGCGTGTGATCTGTGATTTCTCAGGAGCCCTAGAGGA-- 128  
 Qy 181 TGGAAACCAAGAACCTGAAGAGGGAAACAGCAACTCAACGTCAAGCTCAGGATCTCGAGCTG 240  
 Db 129 -----AAAACGTCAAGAGAGGAACCAACCACTGATAATCAGGSTATTCACCTA 178  
 Qy 241 CTCAGGAGGAGAGATGAGGAGCATCTGCAAGTCAAGGCCCGAAGCCTGAAGCTGATA 300  
 Db 179 GTGGGAGATTGAANAATCAAGCTGCTCTTTTCAAGGGCCCTGCATGGAAGCTTTTC 238  
 Qy 301 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGCAGG 360  
 Db 239 AACAGGAACCTGGCTCTCTGTTAAGATAGAGATGAGCCTTGGAGATGGTCTCTGATGTGAGG 298  
 Qy 361 AGATGGACCCGCCAATCCAGAGAGGTGAAGAACCTTGAAGAGGTGAAAGCAATCAC 420  
 Db 299 AGGGTATTATGCGCCACTTTTGTATCTCACTAAAGTGTGAAGAGCAGGTGATCGGCAACAT 358  
 Qy 421 AGTCTTAAAGAGGACAGT-----TGAATGATGAGGCTGCTCTTATGTGTGGAATTT 474  
 Db 359 AGGTTTCAAGCAAGACAAATGAAGACTGAACCAAGAACGTTATCTTAATCTGGAATTT 418

Db 349 TCAAGCAGACAAATGAAGACTGAACCAAGAACGTTATTCTTAATCTGGAATTTGACT 408  
QY 480 ATTAAATTTCTCCCAATAAAGCTTTTA 505  
Db 409 GATATATTTCTCTTAATAAAGTTTA 434

RESULT 11

US-09-970-607-43  
; Sequence 43, Application US/09970607  
; GENERAL INFORMATION:  
; APPLICANT: Malyankar et al.  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-675 CIP2  
; CURRENT APPLICATION NUMBER: US/09/970,607  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 60/182,733  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/182,724  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/183,896  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/184,497  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/224,157  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/184,482  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,744  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/197,083  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/233,405  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 60/236,060  
; PRIOR FILING DATE: 2000-09-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 448  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-970-607-43

Query Match 21.0%; Score 111.6; DB 5; Length 448;  
Best Local Similarity 57.0%; Pred. No. 4.4e-24;  
Matches 254; Conservative 0; Mismatches 174; Indels 18; Gaps 2;  
QY 66 GTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTAT 125  
Db 1 GTGGGAATATGAGTGAGCTTTGTAAGAGCAAGATCCCAATCCTCAGAAAGAGGAATGAC 60  
QY 126 GTACAGCTCTTGAAGTGAATGGGCTATGGCCCTAGGAGCTTCAGTGATCAAGTGAA 185  
Db 61 CAAGAGTCTTCCCGAGCGGTGGATCTGTGATTTCCAGGAGCCCACTGAGGA----- 113  
QY 186 CCAGCAACACCTGAAGAAGGGGAAACAGCAACTCAACCTCAGGATTCCTGAGCTGCTCAG 245  
Db 114 -----AAACGTCAGAGAGAGGAAACCAACTGATATCAGGGTATTGCACCTAGTGGG 168  
QY 246 GAGGAGAGGATGAGGAGGAGCATCTCAGGTCTAAGGGCCGAGCCCTGAAGCTGATAGCCAG 305  
Db 169 GAGATCGAAATGAAGGAGCACTGCCGTTCAAGGCGCTGACATGGAAGCTTTTCAACAG 228  
QY 306 GAACAGGGTCAACCAAGAGTGGGTGAGATGAGATGGTCTGATGGGAGGAGATG 365  
Db 229 GAACCTGGCTCTCTTAAAGATAGAGATGAGCTTGAGATGGTCTGATGAGGAGGGT 288  
QY 366 GACCCGCCAAATCCAGAGGAGGTGAAACGCTGGAAGAGGTGAAAGCAATCACAAGTGT 425  
Db 289 ATTATGCCACCTTTTGTATCTCACTAAAGTGTGGAAGAGGATGATCGCAACCATAGGTT 348

QY 475 TGTTCAATTAATTTCCCAATAAAGCTTTAGAGCTTTCTGCAAGCAAAAAA 532  
Db 419 TGACTGATAATATTTCTTAATAAAGTTTA-AGTTTCTGCAAGAAATCTTCAAAA 475

RESULT 10

US-09-970-607-44  
; Sequence 44, Application US/09970607  
; GENERAL INFORMATION:  
; APPLICANT: Malyankar et al.  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-675 CIP2  
; CURRENT APPLICATION NUMBER: US/09/970,607  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 60/182,733  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/182,724  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/183,896  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/184,497  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/224,157  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/184,482  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,744  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/197,083  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/233,405  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 60/236,060  
; PRIOR FILING DATE: 2000-09-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 448  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-970-607-44

Query Match 22.2%; Score 118; DB 5; Length 448;  
Best Local Similarity 57.8%; Pred. No. 4.6e-26;  
Matches 258; Conservative 0; Mismatches 170; Indels 18; Gaps 2;  
QY 66 GTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTAT 125  
Db 1 GTGGGAATATGAGTGAGCATGTGAGAACAGATCCCAATCCTCAGAAAGAGGAATGAC 60  
QY 126 GTACAGCTCTTGAAGTGAATGGGCTATGGCCCTAGGAGCTTCAGTGATCAAGTGAA 185  
Db 61 CAAGAGTCTTCCCGAGCGGTGGATCTGTGATTTCCAGGAGCCCACTGAGGA----- 113  
QY 186 CCAGCAACACCTGAAGAAGGGGAAACAGCAACTCAACCTCAGGATTCCTGAGCTGCTCAG 245  
Db 114 -----AAACGTCAGAGAGAGGAAACCAACTGATATCAGGGTATTGCACCTAGTGGG 168  
QY 246 GAGGAGAGGATGAGGAGGAGCATCTGAGGTCAAGGGCCGAGCCCTGAAGCTGATAGCCAG 305  
Db 169 GAGATCGAAATGAAGGAGCACTGCCGTTCAAGGCGCTGACATGGAAGCTTTTCAACAG 228  
QY 306 GAACAGGGTCAACCAAGAGTGGGTGAGATGAGATGGTCTGATGGGAGGAGATG 365  
Db 229 GAACCTGGCTCTCTTAAAGATAGAGATGAGCTTGAGATGGTCTGATCAGGAGGGG 288  
QY 366 GACCCGCCAAATCCAGAGGAGGTGAAACGCTGGAAGAGGTGAAAGCAATCACAAGTGT 425  
Db 289 ATTATGCCACCTTTTGTATCTCACTAAAGTGTGGAAGAGGATGATCGCAACCATAGGTT 348  
QY 426 TAAAGAGAGGACGT-----TGAAATGATGACAGGCTGCTCTTATGTTGAAATTTGTTTC 479







Db 231 CTGGCTCTGCTTAAGATAGAGGATGAGCCTGGAGATGGTCCTGATGTCAGGAGGGGATT 290  
Qy 369 CCGCCAAATCCAGAGGAGGTGAATAACGCTGAAGAAGGTGAATAAGCAATCAAG 422  
Db 291 ATGCCCACTTTTGATCTCACTAAGTGTGGAAGCAGGTGATGCGCAACCATAG 344

Search completed: August 6, 2004, 21:54:17  
Job time : 375 secs

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2004, 11:07:15 ; Search time 3602 Seconds  
(without alignments)  
6485.812 Million cell updates/sec

Title: US-09-782-745-18  
Perfect score: 539  
Sequence: 1 GCCAGGAGCTGTGAGGAG.....CTGCAAAAAAAAAAAAAA 539

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 3985670

Minimum DB seq length: 0  
Maximum DB seq length: 539

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2:	gb_htg.*	
3:	gb_in.*	
4:	gb_om.*	
5:	gb_ov.*	
6:	gb_pat.*	
7:	gb_ph.*	
8:	gb_pl.*	
9:	gb_pr.*	
10:	gb_ro.*	
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12:	gb_sy.*	
13:	gb_un.*	
14:	gb_vl.*	
15:	em_ba.*	
16:	em_fun.*	
17:	em_hum.*	
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27:	em_sts.*	
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31:	em_htg_inv.*	
32:	em_htg_other.*	
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38:	em_sy.*	
39:	em_htgo_hum.*	
40:	em_htgo_mus.*	
41:	em_htgo_other.*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	539	100.0	539	6	AR028492 Sequence
2	539	100.0	539	6	BD231801 Isolated
3	539	100.0	539	6	I55855 Sequence 18
4	539	100.0	539	6	BD132471 Isolated,
5	527.2	97.8	532	6	AR028491 Sequence
6	527.2	97.8	532	6	BD231800 Isolated
7	527.2	97.8	532	6	I55854 Sequence 17
8	527.2	97.8	532	6	BD132470 Isolated,
9	527	97.8	527	9	HSU19147 Human GAGE-
10	522.2	96.9	528	6	AX334151 Sequence
11	522.2	96.9	528	9	HSU19145 Human GAGE-
12	519.2	96.3	524	9	HSU19146 Human GAGE-
13	515.2	95.6	524	9	AF058988 Homo sapi
14	510.2	94.7	538	6	AR028488 Sequence
15	510.2	94.7	538	6	BD231797 Isolated
16	510.2	94.7	538	6	I55851 Sequence 14
17	510.2	94.7	538	6	BD132467 Isolated,
18	504	93.5	526	6	AR275666 Sequence
19	504	93.5	526	9	AF055474 Homo sapi
20	502.8	93.3	528	6	AR275665 Sequence
21	502.8	93.3	528	9	AF055473 Homo sapi
22	502.2	93.2	530	9	HSU19143 Human GAGE-
23	356.2	66.1	430	6	AX886264 Sequence
24	356.2	66.1	430	6	BD025874 Sequence
25	303	56.2	530	6	AX284300 Sequence
26	300.8	55.8	365	6	AX284692 Sequence
27	175.8	32.6	493	9	HSB318881 Homo sapi
28	173.2	32.1	494	6	AX921771 Sequence
29	156	28.9	506	6	AR415772 Sequence
30	156	28.9	506	6	BD111325 EST and e
31	152.2	28.2	441	12	BT007722 Synthetic
32	139.2	25.8	494	6	AR416094 Sequence
33	139.2	25.8	494	6	BD111647 EST and e
34	136.6	25.3	500	9	BC054022 Homo sapi
35	134.8	25.0	475	6	AX226497 Sequence
36	131.2	24.3	524	6	AR416095 Sequence
37	131.2	24.3	524	6	BD111648 EST and e
38	121.2	22.5	448	6	AX226538 Sequence
39	114.8	21.3	448	6	AX226537 Sequence
40	113	21.0	529	9	BC009538 Homo sapi
41	109.6	20.3	399	6	AR272357 Sequence
42	109.6	20.3	399	6	AR275938 Sequence
43	109.6	20.3	399	6	AR406213 Sequence
44	109.6	20.3	399	6	AX062442 Sequence
45	109.6	20.3	399	6	AX367359 Sequence

ALIGNMENTS

RESULT 1	AR028492	Sequence 18 from patent US 5858689.	539 bp	DNA	linear	PAT 29-SEP-1999
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DEFINITION	AR028492	Sequence 18 from patent US 5858689.				
ACCESSION	AR028492	Sequence 18 from patent US 5858689.				
VERSION	AR028492.1	GI:5940465				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 539)					
AUTHORS	van der Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Palleur,T.					
TITLE	Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof					



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	/db_xref="taxon:32630"	
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Best Local Similarity	100.0%;	Pred. No. 3.2e-128;
Matches 539; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
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QY	121	CCAAGCGCTATGTACAGCCTCTGAAAGTGAATTGGCCCTATGCGGCCCGAGCAGTTTCAGT 180
Db	121	CCAAGCGCTATGTACAGCCTCTGAAAGTGAATTGGCCCTATGCGGCCCGAGCAGTTTCAGT 180
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Db	241	GCAGCTGTCTCAGAGGGAGGAGTGCAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAA 300
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Db	301	GCTGATAGCCAGAAACAGGCTCACCACACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360
QY	361	GGCGAGGAGTGGACCCGCAAAATCCAGAGGAGTGAAGAGGCTCAAGAGGTGAAAG 420
Db	361	GGCGAGGAGTGGACCCGCAAAATCCAGAGGAGTGAAGAGGCTCAAGAGGTGAAAG 420
QY	421	CAATCACAGTGTAAAGAAAGACACGTTGAAATGATGCGAGGTGCTTCCTATTGTGAAAT 480
Db	421	CAATCACAGTGTAAAGAAAGACACGTTGAAATGATGCGAGGTGCTTCCTATTGTGAAAT 480
QY	481	TTGTTCAATTAATTTCTCCCAATAAGCTTTTACAGCCTTCTGCAAAAAAATAAAAA 539
Db	481	TTGTTCAATTAATTTCTCCCAATAAGCTTTTACAGCCTTCTGCAAAAAAATAAAAA 539
RESULT 5		
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LOCUS	AR028491 532 bp DNA linear PAT 29-SEP-1999	
DEFINITION	Sequence 17 from patent US 5858689.	
ACCESSION	AR028491	
VERSION	AR028491.1 GI:5940464	
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 532)	
AUTHORS	van der Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Falleur,T.	
TITLE	Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof	
JOURNAL	Patent: US 5858689-A 17 12-JAN-1999;	
FEATURES	Location/Qualifiers	
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	/mol_type="unassigned DNA"	
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Best Local Similarity	99.4%;	Pred. No. 3.6e-125;
Matches 529; Conservative	0; Mismatches	3; Indels 0; Gaps 0;
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Best Local Similarity	100.0%;	Pred. No. 3.2e-128;
Matches 539; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
QY	1	GCAGGGAGCTGTGAGGAGTGTGTGTTCTCGCGTCGGACTCTTTTCTCTAC 60
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Db	61	TGAGATTCACTGTGTGAATATGAGTTGCGAGGAAGATCGACCTATTATTGGCCTAGA 120
QY	121	CCAAGCGCTATGTACAGCCTCTGAAAGTGAATTGGCCCTATGCGGCCCGAGCAGTTTCAGT 180
Db	121	CCAAGCGCTATGTACAGCCTCTGAAAGTGAATTGGCCCTATGCGGCCCGAGCAGTTTCAGT 180
QY	181	GATGAAGTGGAAACCCAGCAACACCTGAAGAAAGGGAAACAGAACTCAACGTGAGATCCT 240
Db	181	GATGAAGTGGAAACCCAGCAACACCTGAAGAAAGGGAAACAGAACTCAACGTGAGATCCT 240
QY	241	GCAGCTGTCTCAGAGGGAGGAGTGCAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAA 300
Db	241	GCAGCTGTCTCAGAGGGAGGAGTGCAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAA 300
QY	301	GCTGATAGCCAGAAACAGGCTCACCACACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360
Db	301	GCTGATAGCCAGAAACAGGCTCACCACACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360
QY	361	GGCGAGGAGTGGACCCGCAAAATCCAGAGGAGTGAAGAGGCTCAAGAGGTGAAAG 420
Db	361	GGCGAGGAGTGGACCCGCAAAATCCAGAGGAGTGAAGAGGCTCAAGAGGTGAAAG 420
QY	421	CAATCACAGTGTAAAGAAAGACACGTTGAAATGATGCGAGGTGCTTCCTATTGTGAAAT 480
Db	421	CAATCACAGTGTAAAGAAAGACACGTTGAAATGATGCGAGGTGCTTCCTATTGTGAAAT 480
QY	481	TTGTTCAATTAATTTCTCCCAATAAGCTTTTACAGCCTTCTGCAAAAAAATAAAAA 539
Db	481	TTGTTCAATTAATTTCTCCCAATAAGCTTTTACAGCCTTCTGCAAAAAAATAAAAA 539
RESULT 4		
BD132471		
LOCUS	BD132471 539 bp DNA linear PAT 18-SEP-2002	
DEFINITION	Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof.	
ACCESSION	BD132471	
VERSION	BD132471.1 GI:23227416	
KEYWORDS	JP 2002507112-A/11.	
SOURCE	synthetic construct	
ORGANISM	artificial sequences.	
REFERENCE	1 (bases 1 to 539)	
AUTHORS	Debacker,O., Eynde,B.V.D. and Falleur,T.B.	
TITLE	Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof	
JOURNAL	Patent: JP 2002507112-A 11 05-MAR-2002;	
COMMENT	LUDWIG INSTITUTE FOR CANCER RESEARCH	
	PN JP 2002507112-A/11	
	PD 05-MAR-2002	
	PF 23-JUN-1997 JP 1998503430	
	PR 24-JUN-1996 US 08/669161	
	PI OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIERRY BOON FALLEUR PC	
	A61K38/00,A61K45/05,C07K14/82,C12N15/00 CC	
	Strandedness: Single;	
CC	Topology: Linear;	
PH	Key Location/Qualifiers.	
FEATURES	Location/Qualifiers	
source	1..539	
	/organism="synthetic construct"	

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Qy 68 CATCTGTGTAATATACGATGGCGAGAGATGACCTATTATTGCGCTAGACCAAGGC 127
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Qy 128 GCTATGTACAGCTCTCTGAAGTGTATGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAG 187
Db 121 GCTATGTACAGCTCTCTGAAGTGTATGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAG 180
Qy 188 TGGAAACAGCAACACCTGAAAGAGGAAACAGCAACTCAACGTCAGATCTTCGACGCTG 247
Db 181 TGGAAACAGCAACACCTGAAAGAGGAAACAGCAACTCAACGTCAGATCTTCGACGCTG 240
Qy 248 CTGAGGAGGAGGAGTGGGAGCATCTGAGTGTGAAGTGTGAAGTGTGCTGATGGGCGAGG 307
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Qy 308 GCCAGGAACAGGGTCAACCCACAGACTGGGTGTGAAGTGTGAAGTGTGCTGATGGGCGAGG 367
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Db 361 AGATGGACCCGCCAAATCCAGAGAGGTGAAACCGCTGAAAGAGGTGAAAGCAATCAC 420
Qy 428 AGTGTGTAAGAGACACACGTTGAATGATGACGAGCTGCTCTATGTTGGAATTTGTTCA 487
Db 421 AGTGTGTAAGAGAGGACGTTGAATGATGACGAGCTGCTCTATGTTGGAATTTGTTCA 480
Qy 488 TTAATAATCTCCCAATAAGCTTTACAGCCTTCTGCAAAATTTGCAAAAAA 539
Db 481 TTAATAATCTCCCAATAAGCTTTACAGCCTTCTGCAAAATTTGCAAAAAA 532

RESULT 6
BD231800 532 bp DNA linear PAT 17-JUL-2003
LOCUS Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
DEFINITION as molecules encoding the same, and utilization thereof.
ACCESSION BD231800.1 GI:33041570
VERSION JP 2002509859-A/10.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 532)
AUTHORS Bruggen,P.V.D., Eynde,B.V.D., DeBacker,O. and Falleur,T.B.
TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids
as molecules encoding the same, and utilization thereof
JOURNAL Patent: JP 2002509859-A 10 02-APR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT OS Homo sapiens (human)
PN JP 2002509859-A/10
PD 02-APR-2002
PF 12-JAN-1999 JP 2000528586
PR 23-JAN-1998 US 09/012818
PI PIERRE VAN DER BRUGGEN,BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,
PI THIERRY BOON FALLSUR
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
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FT source 1..532 /organism='Homo sapiens (human)'.
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Best Local Similarity 99.4%; Pred. No. 3.6e-125;
Matches 529; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 8 AGCTGTGAGGCGAGTGTGTGGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 67
Db 1 AGCTGTGAGGCGAGTGTGTGGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60
Qy 68 CATCTGTGTAATATACGATGGCGAGAGATGACCTATTATTGCGCTAGACCAAGGC 127
Db 61 CATCTGTGTGAAATATGATGGCGAGAGATGACCTATTATTGCGCTAGACCAAGGC 120
Qy 128 GCTATGTACAGCTCTCTGAAGTGTATGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAG 187
Db 121 GCTATGTACAGCTCTCTGAAGTGTATGGGCTATGCGGCCCGAGCAGTTCAGTGATGAAG 180
Qy 188 TGGAAACAGCAACACCTGAAAGAGGAAACAGCAACTCAACGTCAGATCTTCGACGCTG 247
Db 181 TGGAAACAGCAACACCTGAAAGAGGAAACAGCAACTCAACGTCAGATCTTCGACGCTG 240
Qy 248 CTGAGGAGGAGGAGTGGGAGCATCTGAGTGTGAAGTGTGAAGTGTGCTGATGGGCGAGG 307
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Db 361 AGATGGACCCGCCAAATCCAGAGAGGTGAAACCGCTGAAAGAGGTGAAAGCAATCAC 420
Qy 428 AGTGTGTAAGAGACACACGTTGAATGATGACGAGCTGCTCTATGTTGGAATTTGTTCA 487
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Qy 488 TTAATAATCTCCCAATAAGCTTTACAGCCTTCTGCAAAATTTGCAAAAAA 539
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RESULT 7
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LOCUS Sequence 17 from patent US 5648226.
ACCESSION I55854
VERSION I55854.1 GI:2476648
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 532)
AUTHORS Van den Eynde,B., DeBacker,O. and Boon-Falleur,T.
TITLE Isolated peptides derived from tumor rejection antigens, and their
use
JOURNAL Patent: US 5648226-A 17 15-JUL-1997;
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source Location/Qualifiers
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ORIGIN
Query Match 97.8%; Score 527.2; DB 6; Length 532;
Best Local Similarity 99.4%; Pred. No. 3.6e-125;
Matches 529; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 8 AGCTGTGAGGCGAGTGTGTGGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 67
Db 1 AGCTGTGAGGCGAGTGTGTGGTTCTCGCGTCCGGACTCTTTTCTCTACTGAGATT 60
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Db      61  CATCTGTGTGAATATGATGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGC 120
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QY      188  TGGACACGACACCTCTGAAGAGGGGAACGAGCAACTCAAGCTCAGGATCCTGCAGCTG 247
Db      181  TGGAACACGACACCTCTGAAGAGGGGAACGAGCAACTCAAGCTCAGGATCCTGCAGCTG 240
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RESULT 8
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LOCUS   BD132470          532 bp    DNA        linear    PAT 18-SEP-2002
DEFINITION Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof.
ACCESSION BD132470
VERSION   BD132470.1 GI:23227415
KEYWORDS  JP 2002507112-A/10.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 532)
AUTHORS   Debacker,O., Bynde,B.V.D. and Falleur,T.B.
TITLE      Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof
JOURNAL    Patent: JP 2002507112-A 10 05-MAR-2002;
COMMENT    LUDWIG INSTITUTE FOR CANCER RESEARCH
PN         JP 2002507112-A/10
PD         05-MAR-2002
PF         23-JUN-1997 JP 1998503430
PI         24-JUN-1996 US 08/669161
PR         OLIVIER DEBACKER,BENOIT VAN DEN EYNDE,THIBERY BOON FALLEUR PC
AG1K38/00,AG1K45/05,C07K14/82,C12N15/00 CC
Strandedness: Single;
CC         Topology: Linear;
FH         Key Location/Qualifiers.
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Query Match      97.8%; Score 527.2; DB 6; Length 532;
Best Local Similarity 99.4%; Pred. No. 3.6e-125;
Matches 529; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      8  AGCTGTGAGGCGAGTGTGTGGTTCCTGCGGTCGAGCATCTTTTTCCTCTACTGAGATT 67
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Db      121  GCTATGTACAGCTCTCTGAAAGTATGGGCTATGCGGCCGAGCAGTTCAGTGTAGAG 180
QY      188  TGGACACGACACCTCTGAAGAGGGGAACGAGCAACTCAAGCTCAGGATCCTGCAGCTG 247
Db      181  TGGAACACGACACCTCTGAAGAGGGGAACGAGCAACTCAAGCTCAGGATCCTGCAGCTG 240
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QY      308  GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGGCGAGG 367
Db      301  GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTATGGGCGAGG 360
QY      368  AGGTGGACCCGCAATCCAGAGGAGGTGAACACCCCTGAAGAAGTGAAGAAGCAATCAC 427
Db      361  AGATGGACCCGCAATCCAGAGGAGGTGAACACCCCTGAAGAAGTGAAGAAGCAATCAC 420
QY      428  AGTGTAAAGAGACACCTTGAAATGATGCGAGGCTGCTCCTATGTGGAATTTGTTCA 487
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QY      488  TTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAAAAA 539
Db      481  TTAATAATCTCCCAATAAGCTTTACAGCTTCTGCAAAAAA 532
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RESULT 9
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LOCUS   Human GAGE-6 protein mRNA, complete cds.
DEFINITION
ACCESSION U19147
VERSION   U19147.1 GI:914908
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
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ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 527)
AUTHORS   Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S. and Boon,T.
TITLE      A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma
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J. Exp. Med. 182 (3), 689-698 (1995)
JOURNAL    MEDLINE
PUBMED     95378788
REFERENCE 2 (bases 1 to 527)
AUTHORS   Van den Eynde,B.J.
TITLE      Direct Submission
JOURNAL    Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
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Query Match 97.8%; Score 527; DB 9; Length 527;  
Best Local Similarity 100.0%; Pred. No. 4e-125;  
Matches 527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	TGAGATTCACTCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGA	120
Db	61	TGAGATTCACTCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCCTAGA	120
QY	121	CCAAGGCGCTTATGTPACAGCTCTCTGAAGTGAATTGGGCTATATGGGCGCCGAGCAGTTCAGT	180
Db	121	CCAAGGCGCTTATGTPACAGCTCTCTGAAGTGAATTGGGCTATATGGGCGCCGAGCAGTTCAGT	180
QY	181	GATGAAGTGAACACAGCAACACCTTGAAGAAGGGGAACAGCAACTCAACGTCAGGATCCT	240
Db	181	GATGAAGTGAACACAGCAACACCTTGAAGAAGGGGAACAGCAACTCAACGTCAGGATCCT	240
QY	241	GCAGCTCTCAGGAGGGAGAGAGATGAGGAGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA	300
Db	241	GCAGCTCTCAGGAGGGAGAGAGATGAGGAGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA	300
QY	301	GCTGTAGCCAGGAAACAGGGTCAACACACAGCTGGGTGTGAGTGTGAAGATGTCCTGAT	360
Db	301	GCTGTAGCCAGGAAACAGGGTCAACACACAGCTGGGTGTGAGTGTGAAGATGTCCTGAT	360
QY	361	GGCGAGAGGTGACCCGCCAAATCCAGAGGAGGTGAAAAACGCTTGAGGAAGGTGAAAAG	420
Db	361	GGCGAGAGGTGACCCGCCAAATCCAGAGGAGGTGAAAAACGCTTGAGGAAGGTGAAAAG	420
QY	421	CAATCACAGTGTGTAAAGAGAGACACGTTGAAATGATGACAGGCTGCTCTATGTTGGAAT	480
Db	421	CAATCACAGTGTGTAAAGAGAGACACGTTGAAATGATGACAGGCTGCTCTATGTTGGAAT	480
QY	481	TTGTTTCATTAAAAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA	527
Db	481	TTGTTTCATTAAAAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA	527

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RESULT 10
AX3344151
LOCUS
DEFINITION
ACCESSION
AX334151
AX334151.1 GI:18124870
KEYWORDS
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS
Young,P.,E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrikan,S., Soppet,D.R. and Weaver,Z.
TITLE
Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL
Patent: WO 0194629-A. 4660 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
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source

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## ORIGIN

Query Match 96.9%; Score 522.2; DB 6; Length 528;  
Best Local Similarity 99.4%; Pred. No. 6.9e-124;  
Matches 524; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GCCAGGAGCTGTGAGCGAGTCTGTGTGGTCTCTGCCGTCGAGATCTCTTTTCCTCTAC 60

[illegible]

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RESULT 11
LOCUS          HSU19145
DEFINITION     Human GAGE-4 protein mRNA, complete cds.
ACCESSION      U19145
VERSION        U19145.1 GI:914904
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S.
and Boon,T.
A new family of genes coding for an antigen recognized by
autologous cytolytic T lymphocytes on a human melanoma
J. Exp. Med. 182 (3), 689-698 (1995)
95378788
7544395
2 (bases 1 to 528)
Van den Eynde,B.J.
Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
1. 528
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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CDS

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Query Match	96.9%; Score 522.2; DB 9; Length 528;
Best Local Similarity	99.4%; Pred. No. 6.9e-124;
Matches 524; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
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Db	242 GCAGCTGCTCAGAGGGAGAGGATGAGGAGCATCTGCAGGTTCAAGGGCCGAAGCTGAA 301
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Db	302 GCTGATAGCCAGGAACTCAGGAGTCAACCAAGTGGGTGTGAGTGTAAGATGGTCTGAT 361
QY	361 GGGCAGGAGTGGACCCGCAATCCAGAGGAGGTGAAACCGCTGAAAGCTGAAAAG 420
Db	362 GGGCAGGAGTGGACCCGCAATCCAGAGGAGGTGAAACCGCTGAAAGCTGAAAAG 421
QY	421 CAATCAGAGTGTAAAGAGACAGTGTGAATGATGAGGCTGCTCTCTATGTTGGAAT 480
Db	422 CAATCAGAGTGTAAAGAGACAGTGTGAATGATGAGGCTGCTCTCTATGTTGGAAT 481
QY	481 TTGTTTCATTAAATTTCTCCCAATAAGCTTTTACAGCTTTCTGCAAAA 527
Db	482 TTGTTTCATTAAATTTCTCCCAATAAGCTTTTACAGCTTTCTGCAAAA 528
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HSU19146	
LOCUS	
Human GAGE-5 protein mRNA, complete cds.	
U19146	
U19146.1 GI:914906	
KEYWORDS	
Homo sapiens (human)	
ORGANISM	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S.	
and Boon,T.	
A new family of genes coding for an antigen recognized by	
autologous cytolytic T lymphocytes on a human melanoma	
J. Exp. Med. 182 (3), 689-698 (1995)	
95378788	
PUBMED	
7544395	
REFERENCE	
2 (bases 1 to 524)	
Van den Eynde,B.J.	
AUTHORS	
Direct Submission	
TITLE	
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute	
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium	
JOURNAL	
FEATURES	
Location/Qualifiers	
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ORIGIN	
Query Match	96.3%; Score 519.2; DB 9; Length 524;
Best Local Similarity	99.4%; Pred. No. 4.1e-123;
Matches 521; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
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QY	128 GCTATGTACAGCTCTCTGAAGTGATTGGGCTTATCGGCCCGAGCAGTTCAGTGATGAAG 187
Db	121 GCTATGTACAGCTCTCTGAAGTGATTGGGCTTATCGGCCCGAGCAGTTCAGTGATGAAG 180
QY	188 TGGAACTGACCAACCTCTGAAGAAAGGGAACTCAAGCAACTCAACCTCAGGATCTCGAGCTG 247
Db	181 TGGAACTGACCAACCTCTGAAGAAAGGGAACTCAAGCAACTCAACCTCAGGATCTCGAGCTG 240
QY	248 CTCAGAGGGAGAGATGAGGAGCATCTGCAGTCAAGGGCCGAAGCTTGAAGCTGATA 307
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QY	308 GCCAGGAACAGGCTCACCCACAGCTGGGTGTGAGTGTGAAGATGCTCTGATGGCCAG 367
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QY	368 AGTGGACCCGCCAAATCCAGAGGAGGTGAAACCGCTTGAAGAGGTGAAAAAGCAATCAC 427
Db	361 AGATGGACCCGCCAAATCCAGAGGAGGTGAAACCGCTTGAAGAGGTGAAAAAGCAATCAC 420
QY	428 AGTGTAAAGAGACACAGTTGAAATGATGAGGCTGCTCTATGTTGGAATTTGTTCA 487
Db	421 AGTGTAAAGAGACACAGTTGAAATGATGAGGCTGCTCTATGTTGGAATTTGTTCA 480
QY	488 TTAATAATTTCTCCCAATAAAGCTTTACAGCTTTCTCAAAAAAAA 531
Db	481 TTAATAATTTCTCCCAATAAAGCTTTACAGCTTTCTCAAAAAAAA 524
RESULT 13	
AF058988	
LOCUS	
Homo sapiens melanoma antigen related GAGE-7 mRNA, complete cds.	
AF058988	
AF058988.1 GI:3300089	
KEYWORDS	
Homo sapiens (human)	
ORGANISM	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Chen,M.E., Lin,S.-H., Chung,L.W.K. and Sikes,R.A.	
Isolation and characterization of PAGE-1 and GAGE-7: new genes	
expressed in the LNCaP prostate cancer progression model that share	

homology with melanoma associated antigens

J. Biol. Chem. (1998) In press

2. (bases 1 to 524)

Chen,M.E., Lin,S.-H., Chung,L.W.K. and Sikes,R.A.

Direct Submission

Submitted (07-APR-1998) Urology, University of Virginia, Box 422,

Charlottesville, VA 22908, USA

Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/cell\_line="LNCap; C4-2"

/note="isolated from prostate cancer cell lines by differential display PCR; expression pattern correlates with progression from androgen sensitive to androgen insensitive in the human prostate cancer progression model LNCap to C4-2"

80. .433

/note="similar to GAGE family of melanoma antigens"

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/product="melanoma antigen related GAGE-7"

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## ORIGIN

Query Match 95.6%; Score 515.2; DB 9; Length 524;  
Best Local Similarity 98.7%; Pred. No. 4.4e-122;  
Matches 517; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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D 61 AGATTCATCTGTGAAATATGCTTGGCGAGGAGATGCACTTATTGGCCCTAGACC 120
QY 123 AAGCGCTATATACAGCTCTCTGAACTGATTGGCCCTATGCGGCCGAGCACTTCACTGA 182
D 121 AAGCGCTATATACAGCTCTCTGAACTGATTGGCCCTATGCGGCCGAGCACTTCACTGA 180
QY 183 TGAAGTGAACACGACCTGTAAGAGGGGACCACTCAACGTGAGATCTCTG 242
D 181 TGAAGTGAACACGACCTGTAAGAGGGGACCACTCAACGTGAGATCTCTG 240
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D 241 AGCTGCTCAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGCGGAGCTTGAAGC 300
QY 303 TGATAGCCAGGAACAGGCTCAACACAGCTGGGTGTGAGTGTGAAGATGCTCTGATGG 362
D 301 TCATAGCCAGGAACAGGCTCAACACAGCTGGGTGTGAGTGTGAAGATGCTCTGATGG 360
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D 361 GCAGAGGTGACCGCCCAATTCAGAGGAGTGAACCGCTGAAGAGGTGAAGCA 420
QY 423 ATCACAGTGTAAAGAGACACAGCTTGAATATGATGAGGCTGCTCTTATGTAATTT 482
D 421 ATCACAGTGTAAAGAGGACAGCTTGAATATGATGAGGCTGCTCTTATGTAATTT 480
QY 483 GTTCATTAATAATTCCTCAATAAAGCTTTACAGCTTCTGCAAA 526
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## RESULT 14

AR028488 538 bp DNA linear PAT 29-SEP-1999  
LOCUS

## DEFINITION

Sequence 14 from patent US 5858689.

ACCESSION AR028488

VERSION AR028488.1 GI:5940461

KEYWORDS

SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 538)

AUTHORS van der Bruggen,P., van den Eynde,B., DeBacker,O. and

Boon-Falleur,F.

TITLE Isolated peptides derived from the gage tumor rejection antigen

precursor and uses thereof

JOURNAL Patent: US 5858689-A 14 12-JAN-1999;

FEATURES Location/Qualifiers

source 1. .538

/organism="unknown"

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## ORIGIN

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Best Local Similarity 98.0%; Pred. No. 8.7e-121;  
Matches 528; Conservative 0; Mismatches 8; Indels 3; Gaps 1;  
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D 3 GCCAGGAGCTGTGAGCAGTGTGTGTCTCTGCGTCCGACCTCTTTTCTCTAC 62  
QY 61 TGAGATTCATCTGTGAAATATGAGTTGGGAGAGATGACCTATTATGGCCCTAGA 120  
D 63 TGAGATTCATCTGTGAAATATGAGTTGGGAGAGATGACCTATTATGGCCCTAGA 119  
QY 121 CCAAGGCGCTATGTACAGCTCTCTGAAAGTGAATGGGCTATGCGGCCGAGCAGTTCAGT 180  
D 120 CCAAGCGCTACGTAGAGCTCTCTGAAATGATTTGGGCTATGCGGCCGAGCAGTTCAGT 179  
QY 181 GATGAAGTGAACCCAGCAACACCTGAAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 240  
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D 240 GCAGCTCTCAGGAGGAGAGGATGAGGAGCATCTCAGGTCAAGGCCGAGCCCTGAA 299  
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D 300 GCTCATAGCCAGNACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 359  
QY 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGAGGTGAAAACGCTTGAAGAGGTGAAAAG 420  
D 360 GGGCAGGAGTGGACCCGCCAAATCCAGAGAGGTGAAAACGCTTGAAGAGGTGAAAAG 419  
QY 421 CAATCAGTGTAAAGAGACACGTTGAAATGATGCAGGCTCTCTATGTTGGAAT 480  
D 420 CAATCAGTGTAAAGAGACACGTTGAAATGATGCAGGCTCTCTATGTTGGAAT 479  
QY 481 TTGTTCAATTAATAATTCCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAA 539  
D 480 TTGTTCAATTAATAATTCCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAA 538
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## RESULT 15

BD231797

LOCUS

DEFINITION BD231797 538 bp DNA linear PAT 17-JUL-2003  
Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
as molecules encoding the same, and utilization thereof.

ACCESSION BD231797

VERSION BD231797.1 GI:33041567

KEYWORDS JP 2002509859-A/7.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 538)

AUTHORS Bruggen,P.V.D., Eynde,B.V.D., Debacker,O. and Falleur,T.B.  
TITLE Isolated polypeptides binding with HLA-A29 molecule, nucleic acids  
as molecules encoding the same, and utilization thereof  
JOURNAL Patent: JP 2002509859-A 7 02-APR-2002;  
LUDWIG INSTITUTE FOR CANCER RESEARCH  
COMMENT OS Homo sapiens (human)  
PN JP 2002509859-A/7  
PD 02-APR-2002  
PF 12-JAN-1999 JP 2000528586  
PR 23-JAN-1998 US 09/012818  
PI PIERRE VAN DEN BRUGEN,BENOIT VAN DEN EYNDE,OLIVIER DERACKER,  
THIERRY BOON FALLEUR  
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC Isolated  
polypeptides binding with HLA-A29 molecule, nucleic CC  
acids as  
CC molecules encoding the same, and utilization thereof FH Key  
FT source Location/Qualifiers  
FT 1. .538 /organism='Homo sapiens (human)'.  
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## ORIGIN

Query Match 94.7%; Score 510.2; DB 6; Length 538;  
Best Local Similarity 98.0%; Pred. No. 8.7e-121;  
Matches 528; Conservative 0; Mismatches 8; Indels 3; Gaps 1;  
QY 1 GCCAGGGAGCTGTGAGGCGAGTCTGTGTGTTCTGTCGCTCCGACTCTTTTTCCTCTAC 60  
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3 GCCAGGGAGCTGTGAGGCGAGTCTGTGTGTTCTGTCGCTCCGACTCTTTTTCCTCTAC 62  
QY 61 TGAGATTCACTGTGTGAATATGATGTTGGGAGGAAGATCGACCTATTATTGGCCTAGA 120  
Db |||||||  
63 TGAGATTCACTGTGTGAATATGATGTTGGGAGGAAGATCGACCTATTATTGGCCTAGA 119  
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Db |||||||  
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Db |||||||  
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Db |||||||  
240 GCAGCTGCTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA 299  
QY 301 GCTGTAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGAAGATGGTCTGTAT 360  
Db |||||||  
300 GCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGAAGATGGTCTGTAT 359  
QY 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGGAGGTGAAACCGCTGAAAGAGTGAAAAAG 420  
Db |||||||  
360 GGGCAGGAGTGGACCCGCCAAATCCAGAGGAGGTGAAACCGCTGAAAGAGTGAAAAAG 419  
QY 421 CAATCACAGTGTAAAGAGACAGTTGAATGATGCGGCTGCTTCCTATGTTGGAAT 480  
Db |||||||  
420 CAATCACAGTGTAAAGAGACAGTTGAATGATGCGGCTGCTTCCTATGTTGGAAT 479  
QY 481 TTGTTCAATTAATAATCTCCCAATAAGCTTTACGCTTCTGCNAAAAAATAAAAAA 539  
Db |||||||  
480 TTGTTCAATTAATAATCTCCCAATAAGCTTTACGCTTCTGCNAAAAAATAAAAAA 538

Search completed: August 7, 2004, 12:46:45  
Job time : 3605 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2004, 11:18:29 ; Search time 2509 Seconds

(without alignments)  
6415.191 Million cell updates/sec

Title: US-09-782-745-18

Perfect score: 539

Sequence: 1 GCCAGGAGCTGTGAGGAG.....CTGCACAAAAA 539

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 28626722

Minimum DB seq length: 0

Maximum DB seq length: 539

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: em\_hcc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_hcc.\*

12: gb\_est3.\*

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14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

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21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_pbg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	503.4	93.4	517	14	CF780547

5	492.4	91.4	509	12	BI868671
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C	450.6	83.6	457	10	AM510753
C	442	82.0	464	9	AA738037
C	440.6	81.7	447	9	AI381509
10	437	81.1	480	12	BG120336
11	436	80.9	505	14	CB115693
C	433.2	80.4	450	9	AA760996
C	418.6	77.7	455	9	AI187350
C	405.8	75.3	418	9	AW016546
C	397.2	73.7	426	9	AA868226
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17	374.4	69.5	445	11	BC005363
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18	362.2	67.2	412	9	AW102587
19	362.2	67.2	412	9	AW102587
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23	315.6	58.6	397	12	BG206349
C	314	58.3	398	9	AA918604
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25	307.8	57.1	320	12	BM836021
26	305.6	56.7	333	13	BU533718
27	274.6	50.9	457	14	CF780497
28	268.2	49.8	275	14	CB147043
29	268.2	49.8	275	14	CB150355
30	268.2	49.8	275	14	CB157288
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31	245.6	45.6	256	12	BG181480
32	230.2	42.7	258	12	BG186708
33	225	41.7	253	12	BG184057
34	225	41.7	253	12	BG184057
35	221.6	41.1	245	12	BG212621
36	218.2	40.5	292	12	BG213622
37	214.8	39.9	245	12	BG208433
C	210.8	39.1	507	9	AA972716
39	207	38.4	256	12	BG216461
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C	193.8	36.0	197	9	AI968311
C	192.8	35.8	226	12	BG220441
45	192.4	35.7	499	12	BG354572

## ALIGNMENTS

RESULT 1	BM832793	537 bp	linear	EST 06-MAR-2002
LOCUS	K-EST0107334	S5SNU484s1	Homo sapiens	cdna clone S5SNU484s1-8-F10
DEFINITION	5', mRNA sequence.			
ACCESSION	BM832793			
VERSION	BM832793.1	GI:19189202		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 537)			
AUTHORS	Kim.N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.			
TITLE	21C Frontier Korean EST Project 2001			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yusong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 8 row: F column: 10 High quality sequence stop: 537.			

FEATURES  
source

Location/Qualifiers  
1. .537  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="SSNU484s1-8-F10"  
/sex="M"  
/tissue\_type="Stomach"  
/cell\_type="Epithelial"  
/cell\_line="SNU-484"  
/lab\_host="Top10F"  
/clone\_lib="SSNU484s1"  
/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;  
Site 2: NotI; The poly (A) + RNA was decapped with tobacco  
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker  
including EcoRI site by treatment of T4 RNA ligase. The  
first strand cDNA was synthesized from oligo dt-selected  
mRNA by priming with dt-tailed vector. The dt-tailed  
vector was adjusted to have about 60nt. The cDNA vector  
was circularized with E. coli DNA ligase after digestion  
of EcoRI which site is also included in vector. An RNA  
strand converted to a DNA strand by Okayama-Berg method.  
The obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F by electroporation method.  
After analyzing and sequencing about 2,000 ~ 3,000  
colonies in original cDNA library, the abundant cDNAs were  
selected and amplified by PCR reaction using vector region  
primer including T7 promoter as 5' primer and N(drp)14 as  
3' primer. The PCR products were used as template for  
synthesis of biotinylated single stranded RNA by in vitro  
transcription reaction. The synthesized RNA probes were  
hybridized with antisense single stranded cDNAs prepared  
from original library and incubated with avidin-gel.  
After removing DNA-RNA hybrids by centrifuge, the  
subtracted cDNA libraries were constructed by  
transformation of the remaining DNA into competent cells E.  
coli Top10F with electroporation method."

## ORIGIN

Query Match 98.7%; Score 532.2; DB 12; Length 537;  
Best Local Similarity 99.4%; Pred. No. 2.8e-98;  
Matches 534; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCAGGAGCGTGTGAGGAGTGTGTGGTCTCGTCGGCGGACCTTTTTCCTCTAC 60  
DB 1 GCCAGGAGCGTGTGAGGAGTGTGTGGTCTCGTCGGCGGACCTTTTTCCTCTAC 60

QY 61 TGAGATTTCATCTGTGTAATATGAGTGTGGGAGATCGACCTATTATTGGCCTAGA 120  
DB 61 TGAGATTTCATCTGTGTAATATGAGTGTGGGAGATCGACCTATTATTGGCCTAGA 120

QY 121 CCAAGGCGCTATGTACAGCCTCTCTGAAGTGAATGGGCGCTATGGCGCCGAGCAGTTCAGT 180  
DB 121 CCAAGGCGCTATGTACAGCCTCTCTGAAGTGAATGGGCGCTATGGCGCCGAGCAGTTCAGT 180

QY 181 GATGAAGTGAACACAGCAACACCTGAAAGAGGGAAACACCACTCAACCTCAGGATCCT 240  
DB 181 GATGAAGTGAACACAGCAACACCTGAAAGAGGGAAACACCACTCAACCTCAGGATCCT 240

QY 241 GCAGCTCTCAGAGGAGAGGATGAGGAGCATCTCAGGTCAAGGCCGAGCCTGAA 300  
DB 241 GCAGCTCTCAGAGGAGAGGATGAGGAGCATCTCAGGTCAAGGCCGAGCCTGAA 300

QY 301 GCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360  
DB 301 GCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360

QY 361 GGGCAGAGGTGACCCGCCAATCCAGAGAGGTGAAACCGCTGAGAGAGGTGAAAG 420  
DB 361 GGGCAGAGGTGACCCGCCAATCCAGAGAGGTGAAACCGCTGAGAGAGGTGAAAG 420

QY 421 CAATCAGTGTAAAAGAGACACGTTGAAATGATGACGCTGCTCTATGTTGGAAT 480  
DB 421 CAATCAGTGTAAAAGAGACACGTTGAAATGATGACGCTGCTCTATGTTGGAAT 480

## Db

421 CAATCAGTGTAAAAGAGACACGTTGAAATGATGACGCTGCTCTATGTTGGAAT 480  
QY 481 TTGTTTCATTAATAATCTCCCAATAAAGCTTTACAGCCTCTCGCAAAAAA 537  
DB 481 TTGTTTCATTAATAATCTCCCAATAAAGCTTTACAGCCTCTCGCAAAAAA 537

## RESULT 2

## BI826605

LOCUS 603077056F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:516892 5',  
DEFINITION mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## COMMENT

## COMMENT

## COMMENT

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## COMMENT

## ORIGIN

Query Match 94.5%; Score 509.4; DB 12; Length 527;  
Best Local Similarity 97.9%; Pred. No. 1.2e-93;  
Matches 516; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 10 CTGTGAGGCGAGTCTGTGTGGTTCCTGCGCGTCTCTTTTCTCTACTGAGATCA 69  
DB 1 CTGTGAGGCGAGTCTGTGTGGTTCCTGCGCGTCTCTTTTCTCTACTGAGATCA 60

QY 70 TCTGTGTGAATATGAGTGTGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGCGC 129  
DB 61 TCTGTGTGAATATGAGTGTGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGCGC 120

QY 130 TATGTACAGCCTCTCTGAAAGTATTGGCGCTTATGCGGCCGAGCAGTTCAGTGAAGTG 189  
DB 121 TATGTACAGCCTCTCTGAAAGTATTGGCGCTTATGCGGCCGAGCAGTTCAGTGAAGTG 180

QY 190 GRACCAAGCACCTCAAGAGGGGAACCAAGCACTCAACCTCAGATCTCTGAGCTGCT 249  
DB 181 GAACCAAGCACCTCAAGAGGGGAACCAAGCACTCAACCTCAGATCTCTGAGCTGCT 240

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QY 250 CAGGAGGAGGATGAGGAGGATCTGCAGGCTCAAGGGCCGAGCCTGAAGCTGTATGC 309
|
|
|
Db 241 CAGAGGGAGAGATGAGGAGGATCTGCAGGCTCAAGGGCCGAGCCTGAAGCTGTATGC 300
|
|
|
QY 310 CAGGAACAGGGTCACCCACACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGCGAGGAG 369
|
|
|
Db 301 CAGGAACAGGGTCACCCACACAGACTGGGTGTGAGTGTGAAGATGGTCTCTGATGGCGAGGAG 360
|
|
|
QY 370 GTGACCCCGCAATCCAGAGGAGGTGAAACGCTGGAAGAGGTGAAAGCAATCACAG 429
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|
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Db 361 ATGGACCCCGCAATCCAGAGGAGGTGAAACGCTGGAAGAGGTGAAAGCAATCACAG 420
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|
|
QY 430 TGTATAAAGAAACACGTTGAAATGATGCAGGCTGCTCTATCTGTGCAATTTGTTCAATT 489
|
|
|
Db 421 TGTATAAAGAAAGCACTGTTGAAATGATGCAGGCTGCTCTATCTGTGCAATTTGTTCAATT 480
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|
|
QY 490 AAAATTTCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAA 536
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|
Db 481 AAAATTTCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAA 527
|
|
|
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RESULT 3
BX108227
LOCUS
DEFINITION
  BX108227 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE998K213161 ;
  IMAGE:1256204, mRNA sequence.
ACCESSION
  BX108227
VERSION
  BX108227.1 GI:27835080
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Organism
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 521)
  Ebert,L., Heil,O., Hennig,S., Neubert,P., Patsch,E., Peters,M.,
  Radelof,J., Schneider,D. and Korn,B.
  Human Unigeneset - RZPD3
  Unpublished (2003)
  Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
  RZPD; IMAGp998K213161.
  RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
  Human Unigeneset - RZPD3 (RZPDLIB No.972)
  http://www.rzpd.de/CloneCards/cgi-
  bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Heubnerweg 6, D-14059 Berlin, Germany
  Tel: +49 30 32639 101
  Fax: +49 30 32639 111
  www.rzpd.de
```

```
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTACACAGGAACAGCTATGAC.
Location/Qualifiers
  1..521
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGp998K213161 ; IMAGE:1256204"
  /tissue_type="pooled germ cell tumors"
  /lab_host="DH10B"
  /clone_lib="NCI_CGAP GC3"
  /note="Vector: pTV73D-Pac (Pharmacia) with a modified
  polylinker; 1st strand cDNA was prepared from 3 pooled
  germ cell tumors, and was then primed with a Not I -
  oligo(dT) primer. Double-stranded cDNA was ligated to Eco
  RI adaptors (Pharmacia), digested with Not I and cloned
  into the Not I and Eco RI sites of the modified pTV73
  vector. Library is not normalized. Library was
  constructed by Bento Soares and M. Fatima Bonaldo."
```

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FEATURES
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    /organism="Homo sapiens"
    /mol_type="mRNA"
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    /clone="IMAGp998K213161 ; IMAGE:1256204"
    /tissue_type="pooled germ cell tumors"
    /lab_host="DH10B"
    /clone_lib="NCI_CGAP GC3"
    /note="Vector: pTV73D-Pac (Pharmacia) with a modified
    polylinker; 1st strand cDNA was prepared from 3 pooled
    germ cell tumors, and was then primed with a Not I -
    oligo(dT) primer. Double-stranded cDNA was ligated to Eco
    RI adaptors (Pharmacia), digested with Not I and cloned
    into the Not I and Eco RI sites of the modified pTV73
    vector. Library is not normalized. Library was
    constructed by Bento Soares and M. Fatima Bonaldo."
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Query Match 94.4%; Score 508.8; DB 13; Length 521;
Best Local Similarity 98.7%; Pred. No. 1.6e-93;
Matches 513; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 18 CAGTGTGTGTGTTCTCTGCGGTCGCGACTCTTTTCTCTACTGAGATTCATCTGTGTG 77
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|
|
Db 1 CAGTGTGTGTGTTCTCTGCGGTCGCGACTCTTTTCTCTACTGAGATTCATCTGTGTG 60
|
|
|
QY 78 AAATATGAGTTGCGAGGAGATTCGACCTATTATTGCGCTAGACCAAGGCGCTATGTACA 137
|
|
|
Db 61 AAATATGAGTTGCGAGGAGATTCGACCTATTATTGCGCTAGTCCAAAGCGCTATGTACA 120
|
|
|
QY 138 GCCTCTCTGAAGTGAATTTGGGCTATGCGGCCGAGCAGTTCAGTGAATGAATGGAACCCAG 197
|
|
|
Db 121 GCCTCTCTGAATGAATTTGGGCTATGCGGCCGAGCAGTTCAGTGAATGAATGGAACCCAG 180
|
|
|
QY 198 AACACCTGAAGAGGGGAAACCGCAACTCAACCTCAGGATCCTGCAAGCTGCTCAGGAGGG 257
|
|
|
Db 181 AACACCTGAAGAGGGGAAACCGCAACTCAACCTCAGGATCCTGCAAGCTGCTCAGGAGGG 240
|
|
|
QY 258 AGAGGATGAGGAGCATCTGCGAGTCAAGGCGCGAAGCCTGAGCTGTATAGCCAGGAACA 317
|
|
|
Db 241 AGAGGATGAGGAGCATCTGCGAGTCAAGGCGCGAAGCCTGAGCTGTATAGCCAGGAACA 300
|
|
|
QY 318 GGGTCAACCCACAGACTGGGTGTGAGTGTGAAGTGTCTCTGATGGGAGGAGGTGGAACCC 377
|
|
|
Db 301 GGGTCAACCCACAGACTGGGTGTGAGTGTGAAGTGTCTCTGATGGGAGGAGGTGGAACCC 360
|
|
|
QY 378 GCCAATTCAGAGGAGGTGAAAACGCTGAAAGAGTGAAGCAATCACAGTGTAAAAA 437
|
|
|
Db 361 GCCAATTCAGAGGAGGTGAAAACGCTGAAAGAGTGAAGCAATCACAGTGTAAAAA 420
|
|
|
QY 438 GAAGCACGTTGAAATGATGCGAGGCTGCTCTATGTTGAAATTTGTTCAATAATTTCT 497
|
|
|
Db 421 GAAGCACGTTGAAATGATGCGAGGCTGCTCTATGTTGAAATTTGTTCAATAATTTCT 480
|
|
|
QY 498 CCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 537
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|
|
Db 481 CCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 520
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|
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CF780547 517 bp mRNA linear EST 20-OCT-2003
AGENCOURT_15739102 NIH MGC.217 Homo sapiens cDNA clone
IMAGE:30524555 5', mRNA sequence.
CF780547
ACCESSION
  CF780547
VERSION
  CF780547.1 GI:37739989
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Organism
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 517)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Daniela S. Gerhard, Ph.D.
  Office of Cancer Genomics
  National Cancer Institute / NIH
  Bldg. 31 Rm10A07 Bethesda, MD 20892
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: James Martin, University of Iowa
  cDNA Library Preparation: M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: NDAM604 row: e column: 12
  High quality sequence strop: 517.
  Location/Qualifiers
```

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RESULT 4
CF780547
LOCUS
DEFINITION
  CF780547
ACCESSION
  CF780547
VERSION
  CF780547.1 GI:37739989
KEYWORDS
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SOURCE
  Homo sapiens (human)
  Organism
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 517)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Daniela S. Gerhard, Ph.D.
  Office of Cancer Genomics
  National Cancer Institute / NIH
  Bldg. 31 Rm10A07 Bethesda, MD 20892
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: James Martin, University of Iowa
  cDNA Library Preparation: M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: NDAM604 row: e column: 12
  High quality sequence strop: 517.
  Location/Qualifiers
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1. 517
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524555"
/tissue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_217"
/notes="vector: pfx-Asc; Site 1: EcoRI; Site 2: NotI;
Library is oligo-dT primed and directionally cloned.
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoK I adaptor, digested with Not I and then cloned
directionally into pfx-Asc vector. Average insert size
0.5-lkb. Adaptors 5' (AATTCGGCAGGAGG) 3' and 5'd
(CCTCGGCGG) 3'. 3' linker sequence - GCGCGCGCTGAGAGCC T18.
Sequencing primers 3' end: T3 promoter primer 5'd
(ATTAACCTCACTTAAGGA) 3'. 5' End: T7 promoter primer 5'd
(ATAACCTCACTTAAGG) 3'. Average insert size 0.5-lkb.
Library was constructed in the laboratory of M. Bento
Soares. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 93.4%; Score 503.4; DB 14; Length 517;
Best Local Similarity 98.8%; Pred. No. 2e-92; 6; Indels 0; Gaps 0;
Matches 507; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 12 GTGAGGAGTCTGTGTGTTCTTCGCGTCCGGACTCTTTTCTCTACTGAGATTCATC 71
Db 4 GAGGGGAGTCTGTGTGTTCTTCGCGTCCGGACTCTTTTCTCTACTGAGATTCATC 63

Qy 72 TGTGTAAATATGATGTGGCAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTA 131
Db 64 TGTGTAAATATGATGTGGCAGGAAGATCGACCTATTATTGGCTAGACCAAGCGCTA 123

Qy 132 TGTACAGCTCTGAGTGTGGCTATGGCCCTATGGCCCGGAGCAGTTCACTGATGAAGTGA 191
Db 124 TGTACAGCTCTGAGTGTGGCTATGGCCCGGAGCAGTTCACTGATGAAGTGA 183

Qy 192 ACCAGCAACACTGAAGAAGGGGACCAAGCAACTCAAGTCTGAGGCTCTGAGCTGTCTCA 251
Db 184 ACCAGCAACACTGAAGAAGGGGACCAAGCAACTCAAGTCTGAGGCTCTGAGCTGTCTCA 243

Qy 252 GGAGGAGAGATGAGGAGGATCTGAGGTCAAGGCCGCGGAGCCTGAGCTGATGAGCCA 311
Db 244 GGAGGAGAGATGAGGAGGATCTGAGGTCAAGGCCGCGGAGCCTGAGCTGATGAGCCA 303

Qy 312 GGAACAGGTCAACACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGGT 371
Db 304 GGAACAGGTCAACACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGCAGGAGAT 363

Qy 372 GGACCCGCAATCCAGAGGAGGTGAAACCGCTGAAGAAGGTGAAAGCAATCACAGTG 431
Db 364 GGACCCGCAATCCAGAGGAGGTGAAACCGCTGAAGAAGGTGAAAGCAATCACAGTG 423

Qy 432 TTAAGAAGACAGCTTGAATGATGAGGCTGCTCTTATGTTGAAATTTGTTCAATAA 491
Db 424 TTAAGAAGACAGCTTGAATGATGAGGCTGCTCTTATGTTGAAATTTGTTCAATAA 483

Qy 492 AATTTCTCCATTAAGCTTTTACAGCTTCTGCA 524
Db 484 AATTTCTCCATTAAGCTTTTACAGCTTCTGCA 516

RESULT 5
BI868671
LOCUS 603392594Fl NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5',
DEFINITION mRNA sequence.
ACCESSION BI868671
VERSION BI868671.1 GI:16042344
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 509)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM12026 row: 1 column: 24
High quality sequence stop: 509.
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1. 509
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5402663"
/tissue_type="adenocarcinoma, cell_line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 91.4%; Score 492.4; DB 12; Length 509;
Best Local Similarity 98.8%; Pred. No. 3.5e-90;
Matches 496; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCACGGAGCTGTGAGGAGTGTGTGTGTTCTTCGCGTCCGGACTCTTTTCTCTAC 60
Db 8 GCTAGGAGCTGTGAGGAGTGTGTGTGTTCTTCGCGTCCGGACTCTTTTCTCTAC 67

Qy 61 TGACATTTCATCTGTGTAATATATCAGTTGGCAGGAAGATCGACTATTATTGGCTAGA 120
Db 68 TGACATTTCATCTGTGTAATATATCAGTTGGCAGGAAGATCGACTATTATTGGCTAGA 127

Qy 121 CCAAGGCGCTATGTACAGCTCTCTGAAGTGAATGGGCTATGCGGCCGAGCAGTTCAGT 180
Db 128 CCAAGGCGCTATGTACAGCTCTCTGAAGTGAATGGGCTATGCGGCCGAGCAGTTCAGT 187

Qy 181 GATGAAGTGNACCAAGCAACCTGAAGAAGGGGAACCAAGCACTCAAGTCAAGATCCT 240
Db 188 GATGAAGTGNACCAAGCAACCTGAAGAAGGGGAACCAAGCACTCAAGTCAAGATCCT 247

Qy 241 GCAGTGTCTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA 300
Db 248 GCAGTGTCTCAGGAGGAGAGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA 307

Qy 301 GCTGATAGCCAGGAACAGGGTCAACCCAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360
Db 308 GCTGATAGCCAGGAACAGGGTCAACCCAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 367

Qy 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGAGTGAACCCCTGAAGAAGGTGAAGAAG 420
Db 368 GGGCAGGAGTGGACCCGCCAAATCCAGAGAGTGAACCCCTGAAGAAGGTGAAGAAG 427

Qy 421 CAATCACAGTGTAAAAAGAGACACGTTGTAATGATGAGGCTGCTCTCTATGTTGGAAT 480
Db 428 CAATCACAGTGTAAAAAGAGACACGTTGTAATGATGAGGCTGCTCTCTATGTTGGAAT 487

Qy 481 TTGTTTCAATAAATTTCTCCCA 502
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```

Db      488 TTGTTCAATTAATAATTCCTCCAA 509
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AA447559      489 bp      mRNA      linear      EST 04-JUN-1997
LOCUS      zw81e11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:782636
DEFINITION      3', similar to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ;, mRNA
sequence.
ACCESSION      AA447559
VERSION      AA447559.1 GI:2161229
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 489)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
JOURNAL      WashU-Merck EST Project 1997
COMMENT      Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 427.
FEATURES
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    /lab_host="DH10B"
    /clone_lib="Soares testis NHT"
    /note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo (dT)
primer [5'
TGTATCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match      87.5%; Score 471.6; DB 9; Length 489;
Best Local Similarity 99.0%; Pred. No. 6.1e-86;
Matches 485; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY      41 CCGGACTCTTTTCTCTACTGAGATTCTGTGTGAATATGAGTTGGCGAGGAAGAT 100
Db      489 CCGGACTCTTTTCTCTACTGAGATTCTGTGTGAATATGAGTTGGCGAGGAAGAT 430
QY      101 CGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCTCTCTGAAGTGAATTGGGCCCTA 160
Db      429 CGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCCTCTCTGAAGTGAATTGGGCCCTA 371
QY      161 TGGGGCCCGGACAGTTCAGTGTAGTGAAGTGAACAGCAACCTGAAGAGGGGAACAG 220
Db      370 TGGGGCCCGGACAGTTCAGTGTAGTGAAGTGAACAGCAACCTGAAGAGGGGAACAG 311
QY      221 CAACTCAAGTCAGGATCTCGAGCTGCTCAGGAGGGAGGATGAGGAGCATCTGCAG 280
|||||
Db      310 CAACTCAAGTCAGGATCTCGAGCTGCTCAGGAGGGAGGATGAGGAGCATCTGCAG 251
QY      281 GTCAAGGGCGGAGCCTGAAGCTGATAGCCAGCAACAGGGTCAACCCACAGACTGGGTGTG 340
Db      250 GTCAAGGGCGGAGCCTGAAGCTGATAGCCAGCAACAGGGTCAACCCACAGACTGGGTGTG 191
QY      341 AGTGTGAAGATGTTCTGTATGGCGCAGGAGTGGACCCGCCAAATCCAGAGGAGGTGAAAA 400
Db      190 AGTGTGAAGATGTTCTGTATGGCGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAA 131
QY      401 CGCCTCAAGAAGTGAAGCAATCACTGTGTAAAGAGACACCTTGAAATGATGCAG 460
Db      130 CGCCTCAAGAAGTGAAGCAATCACTGTGTAAAGAGACACCTTGAAATGATGCAG 71
QY      461 GCTGCTCTCTATGTTGAAATTTGTTTCATTAATAATTCCTCAATAAAGCTTTACAGCCTTC 520
Db      70 GCTGCTCTCTATGTTGAAATTTGTTTCATTAATAATTCCTCAATAAAGCTTTACAGCCTTC 11
QY      521 TGCATAAAAAA 530
Db      10 TGCATAAAAAA 1
RESULT 7
AWS10753/c
LOCUS      AWS10753
DEFINITION      hd39d05.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2911881 3', similar to SM:GGB4_HUMAN Q13068 GAGE-4 PROTEIN. ;,
mRNA sequence.
ACCESSION      AWS10753
VERSION      AWS10753.1 GI:7148831
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 457)
AUTHORS      NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
FEATURES
    source
    1..457
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:2911881"
    /lab_host="DH10B"
    /clone_lib="Soares NFL T GBC S1"
    /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung Nhlh19W, testis NHT, and B-cell
NCT-CCAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
ORIGIN
Query Match      83.6%; Score 450.6; DB 10; Length 457;
Best Local Similarity 99.1%; Pred. No. 1.2e-81;
Matches 453; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 75 GTGAATATGAGTTGGGAGGAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGT 134  
 Db 457 GTGAATATGAGTTGGGAGGAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGT 398  
 QY 135 ACAGCTCTCGAAGTATGGGCTATGCGGCCGAGCAGTTCAGTGAATGGAAC 194  
 Db 397 ACAGCTCTCGAAGTATGGGCTATGCGGCCGAGCAGTTCAGTGAATGGAAC 338  
 QY 195 AGCAACACCTGAGAGGAGGAGACAGCAACTCAACGTCAGGATCCTCAGCTGCTCAGGA 254  
 Db 337 AGCAACACCTGAGAGGAGGAGACAGCAACTCAACGTCAGGATCCTCAGCTGCTCAGGA 278  
 QY 255 GGGAGAGGATGAGGAGGATCTGAGCTCAAGGCCGAGCCTGAAGCTGATAGCCAGGA 314  
 Db 277 GGGAGAGGATGAGGAGGATCTGAGCTCAAGGCCGAGCCTGAAGCTGATAGCCAGGA 218  
 QY 315 ACAGGTCACCCACAGACTGGGTGAGTGTGAAGATGGTCTGATGGGCGAGGAGTGA 374  
 Db 217 ACAGGTCACCCACAGACTGGGTGAGTGTGAAGATGGTCTGATGGGCGAGGAGTGA 158  
 QY 375 CCGCCCAATCCAGAGGAGGTGAACCGCTGAAGAGGTTGAAGCAATCACAGTGTGA 434  
 Db 157 CCGCCCAATCCAGAGGAGGTGAACCGCTGAAGAGGTTGAAGCAATCACAGTGTGA 98  
 QY 435 AAAGAAGACACGTTGAAATGATGAGGCTGCTCTATGTTGGAATTTGTTCAATAAAT 494  
 Db 97 AAAGAAGACACGTTGAAATGATGAGGCTGCTCTATGTTGGAATTTGTTCAATAAAT 38  
 QY 495 TCTCCCAATAAGCTTTACAGCTTCTGCAAAAAA 531  
 Db 37 TCTCCCAATAAGCTTTACAGCTTCTGCAAAAAA 1

RESULT 8  
 AA738037/c  
 LOCUS  
 DEFINITION  
 nxl5ell.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3',  
 similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.  
 AA738037  
 AA738037.1 GI:2768794  
 EST.  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 464)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)  
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 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 435.  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:1256204"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP GC3"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from 3 pooled  
 germ cell tumors, and was then primed with a Not I -  
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pT7T3  
 vector. Library is not normalized. Library was  
 constructed by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

Query Match 82.0%; Score 442; DB 9; Length 464;  
 Best Local Similarity 97.8%; Pred. No. 6.5e-80;  
 Matches 448; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 82 ATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGACCAAGGCGCTATGTACGCT 141  
 Db 464 ATGAGTTGGCGAGGAGATCGACCTATTATTGGCTAGTCCAGACGCTATGTACGCT 405  
 QY 142 CCTGAAGTGAATGGGCTTATCGGCCCGAGCAGTTCAGTGAATGGAACGACGACCA 201  
 Db 404 CCTGAAGTGAATGGGCTTATCGGCCCGAGCAGTTCAGTGAATGGAACGACGACCA 345  
 QY 202 CCTGAAGAGGGGAACCAAGCAACTCAACGTCAGGATCCTGAGCTGCTCAGGAGGAGAG 261  
 Db 344 CCTGAAGAGGGGAACCAAGCAACTCAACGTCAGGATCCTGAGCTGCTCAGGAGGAGAG 285  
 QY 262 GATGAGGAGGAGCATCTGAGGTCAGGTCGAGGCCGAGCCTGAAGCTGATAGCAGGAACAGGGT 321  
 Db 284 GATGAGGAGGAGCATCTGAGGTCAGGTCGAGGCCGAGCCTGAAGCTGATAGCAGGAACAGGGT 225  
 QY 322 CACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGGAGGAGTGGACCCGCCA 381  
 Db 224 CACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGATGGGAGGAGTGGACCCGCCA 165  
 QY 382 AATCCAGAGGAGTGAAGAGCCCTGAAGAGGTGAAGAGCAATCACAGTGTATAAAGAG 441  
 Db 164 AATCCAGAGGAGTGAAGAGCCCTGAAGAGGTGAAGAGCAATCACAGTGTATAAAGAG 105  
 QY 442 ACAGTTGAAATGATGAGGAGTGTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCA 501  
 Db 104 GCAGTTGAAATGATGAGGAGTGTCTCTATGTTGGAATTTGTTCAATAAATTTCTCCA 45  
 QY 502 ATAAAGCTTTACAGCTTCTGCAAAAAA 539  
 Db 44 ATAAGAGTTTACAGCTTCTGCAAAAAA 7

## RESULT 9

AA1381509/c  
 LOCUS  
 DEFINITION  
 te76b07.x1 Soares NFL T\_GBC S1 Homo sapiens cDNA clone  
 IMAGE:2092597 3', similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;,  
 mRNA sequence.  
 AA1381509  
 AA1381509.1 GI:4194290  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 447)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Insert Length: 497 Std Error: 0.00  
 Seq primer: -40UP from Gibco.  
 Location/Qualifiers  
 1..447  
 /organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2092597"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: p7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CCAP GC51) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
```

ORIGIN

Query Match 81.7%; Score 440.6; DB 9; Length 447;  
Best Local Similarity 99.1%; Pred. No. 1.3e-79;  
Matches 443; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 86 GTTGGCGAGGAGATCGACCTATTATTGGCCCTAGACCAAGGCGCTATGTACAGCTCTCTG 145  
DB |||  
QY 146 AAGTGATGGGCTATGCGGCCGAGCAGTTCAGTGANGAAGTGGAAACAGCAACACCTG 205  
DB |||  
QY 206 AAGAGGGGAACGACCACTCAAGCTCAGGATCTCTGACGCTGTCAGGAGGAGGATG 265  
DB |||  
QY 327 AAGAGGGGAACGACCACTCAAGCTCAGGATCTCTGACGCTGTCAGGAGGAGGATG 268  
DB |||  
QY 266 AGGAGAGCTCTCGAGTCAAGGCGCGAAGCTGAAGCTGATGACCAAGGAACAGGCTCAC 325  
DB |||  
QY 267 AGGAGAGCTCTCGAGTCAAGGCGCGAAGCTGAAGCTGATGACCAAGGAACAGGCTCAC 308  
QY 326 CACAGCTGGGTGAGTGTGAAGTGTCTGTGATGGGAGGAGTGGACCCGCCAATFC 385  
DB |||  
QY 207 CACAGACTGGGTGAGTGTGAAGTGTCTGTGATGGGAGGAGTGGACCCGCCAATC 148  
QY 386 CAGAGGGGTGAACGCTGAGAGGTGAAGCAATCAGAGTGTAAAGAGAGACAC 445  
DB |||  
QY 147 CAGAGGGGTGAACGCTGAGAGGTGAAGCAATCAGAGTGTAAAGAGAGACAC 88  
QY 446 GTTGAATGATGAGGCTCTCTATGTTGGAAATTTGTTCAATAAATTTCTCCCAATAA 505  
DB |||  
QY 87 GTTGAATGATGAGGCTCTCTATGTTGGAAATTTGTTCAATAAATTTCTCCCAATAA 28  
QY 506 AGCTTTACAGCTCTCTGCAAAAAAAA 532  
DB |||

RESULT 10  
BG120336 480 bp mRNA linear EST 30-JAN-2001  
LOCUS NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:4451958 5',  
DEFINITION mRNA sequence.  
ACCESSION BG120336  
VERSION BG120336.1 GI:12613845  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 480)  
AUTHORS NIH-MGC http://imgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://imgc.llnl.gov

Plate: LLAM10239 row: p column: 07

High quality sequence stop: 480.

Location/Qualifiers

source

1. 480

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4451958"

/tissue\_type="adenocarcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_90"

/note="Organ: Liver; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.7 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 81.1%; Score 437; DB 12; Length 480;

Best Local Similarity 98.9%; Pred. No. 6.8e-79;

Matches 440; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 95 GAAGATCGACCTATTATTATTGGCTTAGACCAAGGCGCTATGTACAGCTCTCTGAAGTATG 154

DB 1 GAAGATCGACCTATTATTATTGGCTTAGACCAAGGCGCTATGTACAGCTCTCTGAAGTATG 60

QY 155 GGCCTATGCGGCCGAGCAGTTCAGTGATGAAGTGGAAACCAACACCTGAAGAAGGGG 214

DB 61 GGCCTATGCGGCCGAGCAGTTCAGTGATGAAGTGGAAACCAACACCTGAAGAAGGGG 120

QY 215 AACCAAGCAACTCAAGCTCAGGATCTGAGTCTCAGGAGGAGGAGGAGGAGCAT 274

DB 121 AACCAAGCAACTCAAGCTCAGGATCTGAGTCTCAGGAGGAGGAGGAGGAGCAT 180

QY 275 CTGCAAGTCTAAGGCGCGAGCCTGAAGCTGATGACCGAAGCAAGGTCACCCACAGACTG 334

DB 181 CTGCAAGTCTAAGGCGCGAGCCTGAAGCTGATGACCGAAGCAAGGTCACCCACAGACTG 240

QY 335 GGTGTGAGTGTGAAGATGCTCTGATGGCAGAGGTGACCCGCAATCCAGAGGAGG 394

DB 241 GGTGTGAGTGTGAAGATGCTCTGATGGCAGAGGTGACCCGCAATCCAGAGGAGG 300

QY 395 TGAACAACGCTGAAGAAGGTGAAAAAGCAATCAAGTGTATAAAGAGACACGTTGAAATG 454

DB 301 TGAACAACGCTGAAGAAGGTGAAAAAGCAATCAAGTGTATAAAGAGACACGTTGAAATG 360

QY 455 ATGCAAGGCTGCTCTCTATGTTGAAATTTGTCATTAAATTTCTCCCAATAAAGCTTTACA 514

DB 361 ATGCAAGGCTGCTCTCTATGTTGAAATTTGTCATTAAATTTCTCCCAATAAAGCTTTACA 420

QY 515 GCCTTCTGCAAAAAA 539

DB 421 GCCTTCTGCAAAAAA 445

RESULT 11

LOCUS CB115693

DEFINITION K-ST0159805 L8SCK0 Homo sapiens cDNA clone L8SCK0-8-B09 5', mRNA

sequence.

ACCESSION CB115693

VERSION CB115693.1 GI:27941500

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

CB115693 505 bp mRNA linear EST 28-JAN-2003

LOCUS K-ST0159805 L8SCK0 Homo sapiens cDNA clone L8SCK0-8-B09 5', mRNA

sequence.

ACCESSION CB115693

VERSION CB115693.1 GI:27941500

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 505)  
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.  
 21c Frontier Korean EST Project 2001  
 Unpublished (2002)  
 CONTACT: Kim YS  
 Genom Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 8 row: B column: 09  
 High quality sequence stop: 505.  
 Location/Qualifiers  
 1. 505  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="L8SCK0-8-B09"  
 /sex="M"  
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 /lab\_host="Top10P"  
 /clone\_lib="L8SCK0"  
 /note="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."  
 ORIGIN

Query Match 80.9%; Score 436; DB 14; Length 505;  
 Best Local Similarity 97.8%; Pred. No. 1.1e-78;  
 Matches 442; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
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 Db 19 GTTCTCTGCGCTCGGACTCTTTTCCCTACTGAGATTCATCTGTGTGAATATGAGTTG 78  
 QY 90 GCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGCGCTATGACAGCTCTCTGAAGT 149  
 Db 79 GCGAGGAAGATCGACCTATTATTGGCCCTAGACCAAGCGCTATGACAGCTCTCTGAAT 138  
 QY 150 GATTGGCCCTATGGGCGCGAGCGATTTCAGTGATGAAGTGAACACGACACCTGAAGA 209  
 Db 139 GATTGGCCCTATGGGCGCGAGCGATTTCAGTGATGAAGTGAACACGACACCTGAAGA 198  
 QY 210 AGGGGAACAGCAACTCAAGCTCAGGATCTTGCAGCTGCTCAGGAGGAGGATGAGGG 269  
 Db 199 AGGGGAACAGCAACTCAAGCTCAGGATCTTGCAGCTGCTCAGGAGGAGGATGAGGG 258  
 QY 270 AGCATCTGAGGTCAGGGCCGAGCGCTGAAGCTGATAGCAGCAAGAGTCAACCCACA 329  
 Db 259 AGCATCTGAGGTCAGGGCCGAGCGCTGAAGCTGATAGCAGCAAGAGTCAACCCACA 318  
 QY 330 GACTGGGTGTGAGTGAAGATGTTCTGATGGCAGGAGTGAACCGCCAAATCCAGA 389  
 Db 319 GACTGGGTGTGAGTGAAGATGTTCTGATGGCAGGAGTGAACCGCCAAATCCAGA 378  
 QY 390 GAGGTGAAAACCGCTCAAGAGGTGAAAAGCAATCAAGTGTAAAAGAGACATCTGT 449  
 Db 379 GAGGTGAAAACCGCTCAAGAGGTGAAAAGCAATCAAGTGTAAAAGAGACATCTGT 438  
 QY 450 AAATGATCGAGCTGCTCTCTATGTTGAAATT 481  
 Db 439 AAATGTTGAGCTGCTCTCTATGTTGAAACT 470

RESULT 12

AA760996/c  
 LOCUS  
 nx3208.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1257855 3', similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ; mRNA sequence.  
 AA760996  
 AA760996.1 GI:2809926  
 EST.  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 450)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: -40m13 fwd. RT from Amersham  
 High quality sequence stop: 331.  
 Location/Qualifiers  
 1. 450  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /clone\_lib="NCI CGAP GC4"  
 /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polynucleotide linker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."  
 ORIGIN

Query Match 80.4%; Score 433.2; DB 9; Length 450;  
 Best Local Similarity 98.9%; Pred. No. 4e-78;  
 Matches 446; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 82 ATGAGTTGGCGAGGAGATCGACTATTATTGGCTAGACCAAGCGCTATGTACAGCT 141  
 Db 450 ATGAGTTGGCGAGGAGATCGACTATTATTGGCTAGACCAAGCGCTATGTACAGCT 391  
 QY 142 CCTGAAGTATTGGCCCTATCGCGCCCGAGCAGTTTCAAGTATGAAGTGAACCAAGCA 201  
 Db 390 CCTGAAGTATTGGCCCTATCGCGCCCGAGCAGTTTCAAGTATGAAGTGAACCAAGCA 331  
 QY 202 CCTGAAGAGAGGAAACAGCACTCAACGTTCAGGATCCTCAGTCTCAGGAGGAGAG 261  
 Db 330 CCTGAAGAGAGGAAACAGCACTCAACGTTCAGGATCCTCAGTCTCAGGAGGAGAG 271  
 QY 262 GATGAGGAGCATCTCGCAGGTCAAGGCCGGAAGCCTGAAGTATATGCCAGGAAACAGGT 321  
 Db 270 GATGAGGAGCATCTCGCAGGTCAAGGCCGGAAGCCTGAAGTATATGCCAGGAAACAGGT 211  
 QY 322 CACCCACAGACTCGGTGTGAGTGTGAAGATGGTCTCTATGGCAGGAGGTGGACCCGCCA 381  
 Db 210 CACCCACAGACTCGGTGTGAGTGTGAAGATGGTCTCTATGGCAGGAGGTGGACCCGCCA 151  
 QY 382 AATCCAGAGAGGTGAAACCGCTGAGAGGTGAAAGCAATCACAGTGTAAAGAG 441



NCI CGAP Lu19, NCI CGAP GC4, NCI CGAP GC6, NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonids 132376-132391, 1456008-1456775, 1500552-1502855) NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonids 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI CGAP Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE Clonids 1414920-1417991, 1520904-1522439) NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonids 1257096-1258631, 1459064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonids 985608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE Clonids 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 4 million recombinants. Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG\_TISSUE=germ cell TAG\_LIB=NCI CGAP\_GC4 TAG\_SEQ=AAATC"

ORIGIN

Query Match 75.3%; Score 405.8; DB 9; Length 418; Best Local Similarity 98.3%; Pred. No. 1.5e-72; Matches 410; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 123 AAGCGCTATGTACAGCTCTCTGAAGTGAATGGCCCTATGGCCCGAGCAGTTCAGTGA 182  
DB 418 AAGACGCTAGCTAGAGCTCTCTGAATGAATGGCCCTATGGCCCGAGCAGTTCAGTGA 359

QY 183 TGAAGTGGAAACACCTGACACCTGACAGAGGGGAAACCACTCAACGTGAGGATCTGC 242  
DB 358 TGAAGTGGAAACACCTGACACCTGACAGAGGGGAAACCACTCAACGTGAGGATCTGC 299

QY 243 AGCTGCTCAGGAGGAGGAGTGAAGGAGCATCTGAGGTCAAGGGCGAGCCTGAAGC 302  
DB 298 AGCTGCTCAGGAGGAGGAGTGAAGGAGCATCTGAGGTCAAGGGCGAGCCTGAAGC 239

QY 303 TGATAGCCAGGAACAGGCTACCCACAGACTGGGTGTGAGTGTGAAGTGTCTCTGATGG 362  
DB 238 TCATAGCCAGGAACAGGCTACCCACAGACTGGGTGTGAGTGTGAAGTGTCTCTGATGG 179

QY 363 GCAGGAGGTGGACCCGCCAATCCAGAGGAGGTGAACCGCTGAAGAGGTGAAGCA 422  
DB 178 GCAGGAGGTGGACCCGCCAATCCAGAGGAGGTGAACCGCTGAAGAGGTGAAGCA 119

QY 423 ATCACAGTGTAAAGAGACAGCTGAATGATGAGGCTGCTCTCTATGTTGAAATTT 482  
DB 118 ATCACAGTGTAAAGAGACAGCTGAATGATGAGGCTGCTCTCTATGTTGAAATTT 59

QY 483 GTTCATTAATAATCTCCCAATAAAGCTTTACAGCTTTCTGCAAAAAA 539  
DB 58 GTTCATTAATAATCTCCCAATAAAGCTTTACAGCTTTCTGCAAAAAA 2

RESULT 15  
AA868226/c  
LOCUS  
DEFINITION  
ak48h07.s1 Soares testis NHT Homo sapiens cdna clone IMAGE:1409245  
3' similar to SW:GGE2\_HUMAN Q13066 GAGE-2 PROTEIN. [1]; mRNA  
sequence.  
AA868226.1 GI:2963671  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (Bases 1 to 426)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [CGAPs@mail.nih.gov](mailto:CGAPs@mail.nih.gov)  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

FEATURES  
source

Possible reversed clone: similarity on wrong strand  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 363.  
Location/Qualifiers  
1..426  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1409245"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5].  
TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTT 3'.  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 73.7%; Score 397.2; DB 9; Length 426;  
Best Local Similarity 96.4%; Pred. No. 8.7e-71;  
Matches 405; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 109 TATTGGCTAGACCAAGGCGCTATGTACAGCTCTCTGAGGTGTTGGCGCTATGCGGCC 168  
DB 420 TATCGGCTAGACCAAGGCGCTATGTACAGCTCTCTGAGGTGTTGGCGCTATGCGGCC 361

QY 169 GAGCAGTTCAGTGTGAAGTGGAAACCAAGCAACCTGAAGAGGGGAACCAAGCACTCAA 228  
DB 360 GAGCAGTTCAGTGTGAAGTGGAAACCAAGCAACCTGAAGAGGGGAACCAAGCACTCAA 301

QY 229 CGTCAGGATCCTCAGCTGCTCAGGAGGAGAGATGAGGAGGATCTGAGGTCAAGGG 289  
DB 300 CGTCAGGATCCTCAGCTGCTCAGGAGGAGAGATGAGGAGGATCTGAGGTCAAGGG 241

QY 289 CCGAAGCTCAAGCTGATAGCCAGGACAGGCTCAACACAGAGTGGTGTGAGTGTGAA 348  
DB 240 CCGAAGCTCAAGCTGATAGCCAGGACAGGCTCAACACAGAGTGGTGTGAGTGTGAA 181

QY 349 GATGGTCTCTGATGGGAGGAGTGGACCCGCCAAATCCAGAGGAGTGAAGGCGCTGAA 408  
DB 180 GATGGTCTCTGATGGGAGGAGTGGACCCGCCAAATCCAGAGGAGTGAAGGCGCTGAA 121

QY 409 GAAGGTGAAGCAATCAGTGTAAAGAACACAGCTTGAATGATGAGGCTGTCTCC 468  
DB 120 GAAGGTGAAGCAATCAGTGTAAAGAACACAGCTTGAATGATGAGGCTGTCTCC 61

QY 469 TATGTTGGAATTTGTTTCAATTAATAATCTCCCAATAAAGCTTTACAGCTTTCTGCAAAA 528  
DB 60 TATGTTGGAATTTGTTTCAATTAATAATCTCCCAATAAAGCTTTACAGCTTTCTGCAAAA 1

Search completed: August 7, 2004, 13:28:48  
Job time : 2513 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2004, 08:42:53 ; Search time 390 Seconds  
(without alignments)  
5871.228 Million cell updates/sec

Title: US-09-782-745-18

Perfect score: 539

Sequence: 1 GCCAGGAGCTGTGAGGCAG.....CTGCAAAAAAAAAAAAAA 539

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5022056

Minimum DB seq length: 0

Maximum DB seq length: 539

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 29Jan04: \*  
1: geneseqn1980s: \*  
2: geneseqn1990s: \*  
3: geneseqn2000s: \*  
4: geneseqn2001as: \*  
5: geneseqn2001bs: \*  
6: geneseqn2002s: \*  
7: geneseqn2003as: \*  
8: geneseqn2003bs: \*  
9: geneseqn2003cs: \*  
10: geneseqn2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	529.4	98.2	539	2 AAV18721	AAV18721 cDNA enco
2	527.2	97.8	532	2 AAX90522	Aax90522 GAGE-5 tu
3	527	97.8	527	7 ACC51027	Acc51027 Human bla
4	527	97.8	527	7 ABX76236	Abx76236 Lung canc
5	522.2	96.9	528	6 ABL66323	AbL66323 lung canc
6	519.2	96.3	532	2 AAV18720	AAV18720 cDNA enco
7	510.2	94.7	538	2 AAX90519	Aax90519 GAGE-2 tu
8	504	93.5	526	7 ADA15802	Adal15802 Human GAG
9	502.8	93.3	528	7 ADA15801	Adal15801 Human GAG
10	502.2	93.2	530	7 ABZ220463	Abz20463 GAGE-2 fu
11	468.4	86.9	535	2 AAV18717	AAV18717 cDNA enco
12	356.2	66.1	430	3 AAC02129	Aac02129 Human sec
c 13	303	56.2	530	4 AAS60104	Aas60104 Human can
c 14	300.8	55.8	365	4 AAS60496	Aas60496 Human can
c 15	244	45.3	277	7 ABZ19551	Abz19551 Group III
c 16	242.4	45.0	257	7 ABZ19955	Abz19955 Group III
17	242.4	45.0	264	7 ABZ19755	Abz19755 Group III
18	227.4	42.2	229	7 ABZ20437	Abz20437 TFS1 subt
c 19	227	42.1	227	7 ABZ20480	Abz20480 TFS1 subt
c 20	226	41.9	229	7 ABZ18686	Abz18686 Group III
c 21	218.4	40.5	259	7 ABZ19791	Abz19791 Group III
22	210	39.0	520	7 ABT15737	Abt15737 Human can
23	204	37.8	225	7 ABZ19533	Abz19533 Group III

24	202.4	37.6	509	7 ABX77605	Abx77605 Different
25	202.4	37.6	509	8 ACD42232	AcD42232 Human GAG
26	202.4	37.6	509	9 ADC24646	Adc24646 Human cDN
27	187	34.7	532	4 AAI60530	Aai60530 Human pol
28	178	33.0	219	7 ABZ19538	Abz19538 Group III
29	164.2	30.5	503	5 AAS69484	Aas69484 DNA enco
30	144.8	26.9	528	7 ABT15728	Abt15728 Human can
31	134.8	25.0	475	4 AAD14981	Aad14981 Human NOV
32	129.8	24.1	538	7 ABT15736	Abt15736 Human can
33	109.6	20.3	399	5 AAF68151	Aaf68151 Human lun
34	109.6	20.3	399	6 ABK38062	Abk38062 cDNA enco
35	109.6	20.3	399	7 ACA10391	AcA10391 Human lun
36	109.6	20.3	399	7 ABX99342	Abx99342 Lung canc
37	109.6	20.3	399	10 ADE72125	Ade72125 Human lun
38	105.2	19.5	505	6 AAD24228	Aad24228 Human dif
39	105	19.5	463	6 ABA92217	AbA92217 Melanoma
40	103.2	19.1	515	4 AAH93807	Aah93807 Human pro
41	103.2	19.1	515	4 AAS63900	Aas63900 Human pro
42	103.2	19.1	515	4 AAH02872	Aah02872 Prostate
43	103.2	19.1	515	4 AAH85121	Aah85121 Human pro
44	103.2	19.1	515	5 ACA59708	AcA59708 Prostate
45	103.2	19.1	515	6 ABL95271	Ab195271 Human P10

## ALIGNMENTS

RESULT 1  
AAV18721  
ID AAV18721 standard; cDNA; 539 BP.  
AC AAV18721;  
XX  
XX  
DT 30-JUL-1998 (first entry)  
XX  
DE cDNA encoding GAGE-6 tumour rejection antigen precursor.  
XX  
KW GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;  
KW melanoma; antigen; cytolytic T cell clone proliferation;  
KW HLA-typing assay; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 82..436  
FT /tag= a  
FT /transl\_except= (pos:127..129, aa:Arg)  
FT /transl\_except= (pos:196..198, aa:Ala)  
FT /transl\_except= (pos:199..201, aa:Thr)  
XX  
XX WO9749417-Al.  
PN 31-DEC-1997.  
PD 23-JUN-1997; 97WO-US010850.  
PF 24-JUN-1996; 96US-00669161.  
PR (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX Debacker O, Van Den Eynde B, Boon-Falleur T;  
XX WPI; 1998-076905/07.  
DR P-PSDB; AAW47603.  
XX  
XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -  
PT processed by HLA-Cw6 molecules into peptides, useful to diagnose  
PT melanomas.  
XX  
XX Example 13; Fig 4; 60pp; English.  
XX The present sequence encodes a GAGE-6 tumour tumour rejection antigen  
CC precursor (TRAP). The protein is expressed in a number of tumours. In

CC contrast the only normal tissue which expresses GAGE TRAP protein is  
 CC testis. Several GAGE TRAPs have been identified (see AAV18717-21). The  
 CC major difference between these proteins and GAGE-1 (AAV05540) is the  
 CC absence of a stretch of 143 bases located at position 379 to 521 of the  
 CC GAGE-1 TRAP sequence. The rest of the sequences show mismatches at  
 CC various position, with the exception of GAGE-3 whose 5' end is totally  
 CC different from the other GAGE cDNAs for the first 112 bases. This region  
 CC of GAGE-3 cDNA contains a long repeat and a hairpin structure. The  
 CC antigens can be used to diagnose melanomas, characterised by expression  
 CC of a TRAP or presentation of a tumour rejection antigen. Antigens shed  
 CC into blood or urine can be observed and then used to confirm a diagnosis  
 CC of melanoma using cytolytic T cell clone proliferation methodologies.  
 CC Other uses for the processed peptides, include HLA-typing assays for,  
 CC e.g. skin graft or organ transplants

XX  
 SQ Sequence 539 BP; 157 A; 114 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 98.2%; Score 529.4; DB 2; Length 539;  
 Best Local Similarity 98.9%; Pred. No. 7.1e-139;  
 Matches 533; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCAGGAGCTGTGAGCAGTGTCTGTGTTCTGCGTCCGACCTTTTCTCTAC 60  
 DB 1 GCCAGGAGCTGTGAGCAGTGTCTGTGTTCTGCGTCCGACCTTTTCTCTAC 60  
 QY 61 TGAGATTCACTGTGTGAATATGAGTTGGCGAGGAGATCGACTTATTGGCCCTAGA 120  
 DB 61 TGAGATTCACTGTGTGAATATGAGTTGGCGAGGAGATCGACTTATTGGCCCTAGA 120  
 QY 121 CCAAGGCGCTATGTACAGCTCTCTGAAGTGAATGGGCTATGGGCGCGAGCTTCAGT 180  
 DB 121 CCAAGGCGCTATGTACAGCTCTCTGAAGTGAATGGGCTATGGGCGCGAGCTTCAGT 180  
 QY 181 GATGAAGTGAACAGGAGCTCTCTGAAGTGAATGGGCTATGGGCGCGAGCTTCAGT 240  
 DB 181 GATGAAGTGAACAGGAGCTCTCTGAAGTGAATGGGCTATGGGCGCGAGCTTCAGT 240  
 QY 241 GCAGCTGCTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCGGAGCCCTGAA 300  
 DB 241 GCAGCTGCTCAGGAGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCGGAGCCCTGAA 300  
 QY 301 GCTGATAGCAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGCGGAGCCCTGAA 360  
 DB 301 GCTGATAGCAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGCGGAGCCCTGAA 360  
 QY 361 GGGCAGGAGTGGACCCGCAATCCAGAGGAGTGAACGCTGAAGAGGTGAAG 420  
 DB 361 GGGCAGGAGTGGACCCGCAATCCAGAGGAGTGAACGCTGAAGAGGTGAAG 420  
 QY 421 CAATCAGAGTGTAAAGAGAGACACGTTGAAATGATCAGGCTGCTCCTATGTTGAAAT 480  
 DB 421 CAATCAGAGTGTAAAGAGAGACACGTTGAAATGATCAGGCTGCTCCTATGTTGAAAT 480  
 QY 481 TTGTTCAATTAATCTCCATTAAGCTTTACAGCTTTACAGCTTTCTGCAAAAAA 539  
 DB 481 TTGTTCAATTAATCTCCATTAAGCTTTACAGCTTTCTGCAAAAAA 539

RESULT 2.

AXX90522  
 ID AAX90522 standard; cDNA; 532 BP.

AC AAX90522;

XX 30-SEP-1999 (first entry)

DE GAGE-5 tumour rejection antigen clone nucleotide sequence.

XX Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
 KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
 KW GAGE; ss.

OS Homo sapiens.

XX WO937665-A1.  
 PN 29-JUL-1999.  
 PD 12-JAN-1999; 99WO-US000775.  
 PF 23-JAN-1998; 98US-00012818.  
 PR (LUDW-) LUDWIG INST CANCER RES.  
 PA Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;  
 PI WPI; 1999-469111/39.  
 PT New isolated peptides which bind to HLA-A29 molecules, which are tumor  
 PT rejection antigens used for detection and therapy of pathological  
 PT conditions, e.g. cancer.  
 XX Example 13; Fig 4; 62pp; English.  
 CC The present invention describes peptides which bind to human leukocyte  
 CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into  
 CC tumour rejection antigens. They can be used for detecting cytolytic T  
 CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-  
 CC typing assays. Complexes of HLA-29 molecules and the peptides can be used  
 CC for stimulating CTLs in vivo. The present sequence represents a GAGE  
 CC tumour rejection antigen clone, from an example from the present  
 CC invention

XX SQ Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 U; 0 Other;

Query Match 97.8%; Score 527.2; DB 2; Length 532;  
 Best Local Similarity 99.4%; Pred. No. 2.9e-138;  
 Matches 523; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 AGCTGTGAGCAGTGTGTGTTCTGCGTCCGACCTTTTCTCTACTAGATT 67  
 DB 1 AGCTGTGAGCAGTGTGTGTTCTGCGTCCGACCTTTTCTCTACTAGATT 60  
 QY 68 CATCTGTGAAATATAGTTGGCGAGGAGATCGACCTATTATTGGCCCTAGACCAAGC 127  
 DB 61 CATCTGTGTGAATATAGTTGGCGAGGAGATCGACCTATTATTGGCCCTAGACCAAGC 120  
 QY 128 GCTATGTACAGCTCTCTGAAGTGTGGGCTATGGGCGCGAGCAGTTCAGTGTCAAG 187  
 DB 121 GCTATGTACAGCTCTCTGAAGTGTGGGCTATGGGCGCGAGCAGTTCAGTGTCAAG 180  
 QY 188 TGGAAACCCAGCAACACCTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCCTGCAGCTG 247  
 DB 181 TGGAAACCCAGCAACACCTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCCTGCAGCTG 240  
 QY 248 CTGAGGAGGAGGATGAGGAGCATCTGCAGGTTCAGGCGCGAGCCCTGAAGCTGATA 307  
 DB 241 CTGAGGAGGAGGATGAGGAGCATCTGCAGGTTCAGGCGCGAGCCCTGAAGCTGATA 300  
 QY 308 GCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGCGAG 367  
 DB 301 GCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGATGGGCGAG 360  
 QY 368 AGGTGGACCCGCAAAATCCAGAGGAGTGAAGACCGCTGAAGAGGTGAAGCAATCAC 427  
 DB 361 AGATGGACCCGCAAAATCCAGAGGAGTGAAGACCGCTGAAGAGGTGAAGCAATCAC 420  
 QY 428 AGTGTAAAGAGACACGTTGAATGATGACGCTGCTCTATGTTGGAAATTTGTCA 487  
 DB 421 AGTGTAAAGAGAGGAGCAGTGTGAATGATGACGCTGCTCTATGTTGGAAATTTGTCA 480  
 QY 488 TTAATAATCTCCCAATAAAGCTTTACAGCTTTCTGCAAAAAA 539  
 DB 481 TTAATAATCTCCCAATAAAGCTTTACAGCTTTCTGCAAAAAA 532

```
RESULT 3
ACC51027
ID ACC51027 standard; cDNA; 527 BP.
XX
AC ACC51027;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human bladder cancer associated cDNA sequence SEQ ID NO:144.
XX
KW Human; bladder cancer; cytostatic; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003003906-A2.
XX
PD 16-JAN-2003.
XX
PF 03-JUL-2002; 2002WO-US021338.
XX
PR 03-JUL-2001; 2001US-0302814P.
XX
PR 03-AUG-2001; 2001US-0310099P.
XX
PR 08-NOV-2001; 2001US-0343705P.
XX
PR 13-NOV-2001; 2001US-0350666P.
XX
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Mack DH, Aziz N;
XX
XX WPI; 2003-201532/19.
XX
DR P-PSDB; ABR48213.
XX
PT Detecting a bladder cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT bladder cancer-associated polynucleotide or antibody.
XX
PS Claim 6; Page 279; 307pp; English.
XX
CC The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridizes to a sequence that is 80 % identical to a
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications
XX
SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;

Query Match          97.8%; Score 527; DB 7; Length 527;
Best Local Similarity 100.0%; Pred. No. 3.3e-138;
Matches 527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGAGCTGTGAGGAGCTGTGTGTCTGCTGCGCTCGGACTCTTTTCTCTAC 60
Db 1 GCCAGGAGCTGTGAGGAGCTGTGTGTCTGCTGCGCTCGGACTCTTTTCTCTAC 60
QY 61 TGAGATTCACTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGA 120
Db 61 TGAGATTCACTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCTAGA 120
QY 121 CCAAGCGCTATGTACAGCTCTCTGAAGTGAATTGGCCCTATCGGCCCGAGCAGTTCAGT 180
Db 121 CCAAGCGCTATGTACAGCTCTCTGAAGTGAATTGGCCCTATCGGCCCGAGCAGTTCAGT 180
```

```
QY 181 GATGAAGTGGRACACGACACCTCTGAGAGGGGACCACTCAACGTCAGGATCCT 240
Db 181 GATGAAGTGGAACACGACACCTCTGAGAGGGGACCACTCAACGTCAGGATCCT 240
QY 241 GCAGCTGCTTCAGGAGGAGAGGATGAGGAGGATCTGCAGGTCAGGGCCGAAAGCCTGAA 300
Db 241 GCAGCTGCTTCAGGAGGAGAGGATGAGGAGGATCTGCAGGTCAGGGCCGAAAGCCTGAA 300
QY 301 GCTGATAGCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 360
Db 301 GCTGATAGCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGCTCTGAT 360
QY 361 GGGCAGGAGGTGGACCCGCCAATCCAGAGGAGGTGAAAACGCTTGAAGAGTGAAGAAG 420
Db 361 GGGCAGGAGGTGGACCCGCCAATCCAGAGGAGGTGAAAACGCTTGAAGAGTGAAGAAG 420
QY 421 CAATCACAGTGTAAAAAGAGACAGCTTGAAATGATGCAAGGCTGCTTATGTTGAAAT 480
Db 421 CAATCACAGTGTAAAAAGAGACAGCTTGAAATGATGCAAGGCTGCTTATGTTGAAAT 480
QY 481 TTGTTCAATTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527
Db 481 TTGTTCAATTAATAATCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527

RESULT 4
ABX76236
ID ABX76236 standard; DNA; 527 BP.
XX
AC ABX76236;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #105.
XX
KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
XX WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
XX
PR 10-MAY-2001; 2001US-0290492P.
XX
PR 09-NOV-2001; 2001US-0339245P.
XX
PR 13-NOV-2001; 2001US-0350666P.
XX
PR 29-NOV-2001; 2001US-0334370P.
XX
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
XX WPI; 2003-093161/08.
XX
DR P-PSDB; ABU56512.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 22; Page 273; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
```

to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the invention

SQ Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;

Query Match 97.8%; Score 527; DB 7; Length 527;

Best Local Similarity 100.0%; Pred. No. 3.3e-138;

Matches 527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 GCCAGGAGCTGTGAGCAGTGTGTGTGTTCTGCTCCGTCGACCTTTTTCCTCTAC 60
Db 1 GCCAGGAGCTGTGAGCAGTGTGTGTGTTCTGCTCCGTCGACCTTTTTCCTCTAC 60
Qy 61 TGGATTCATCTGTGTAATATAGTTGGCGAGGAGATCGACCTATTATGGCCTAGA 120
Db 61 TGGATTCATCTGTGTAATATAGTTGGCGAGGAGATCGACCTATTATGGCCTAGA 120
Qy 121 CCAAGGCGCTATGTACAGCCTCTTGAAGTGAATGGGCTATGCGGCCGAGCAGTTCAGT 180
Db 121 CCAAGGCGCTATGTACAGCCTCTTGAAGTGAATGGGCTATGCGGCCGAGCAGTTCAGT 180
Qy 181 GATGAAGTGAACAGCAACACCTTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 240
Db 181 GATGAAGTGAACAGCAACACCTTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCCT 240
Qy 241 GCAGCTCTCAGGAGGAGGAGTGGAGGAGCATCTCAGTCAAGGCCGAGCCTGAA 300
Db 241 GCAGCTCTCAGGAGGAGGAGTGGAGGAGCATCTCAGTCAAGGCCGAGCCTGAA 300
Qy 301 GCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360
Db 301 GCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360
Qy 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGAGTGAAACGCTCGAAGAGGTGAAAG 420
Db 361 GGGCAGGAGTGGACCCGCCAAATCCAGAGAGTGAAACGCTCGAAGAGGTGAAAG 420
Qy 421 CAATCAGAGTGTAAAGAGACACAGTTTGAATCATGAGCTCTCTATGTTGGAAT 480
Db 421 CAATCAGAGTGTAAAGAGACACAGTTTGAATCATGAGCTCTCTATGTTGGAAT 480
Qy 481 TTGTTCTATTAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527
Db 481 TTGTTCTATTAATTTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527
```

RESULT 5

ABL66323

ID ABL66323 standard; DNA; 528 BP.

XX ABL66323;

AC ABL66323;

XX 15-MAY-2002 (first entry)

XX Lung cancer related gene sequence SEQ ID NO:4660.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

XX cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;

gene; ds.

XX Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US010838.

XX 05-JUN-2000; 2000US-0209473P.

XX 05-JUN-2000; 2000US-0209531P.

XX 18-SEP-2000; 2000US-0233133P.

XX 18-SEP-2000; 2000US-0233161P.

XX 20-SEP-2000; 2000US-0234009P.

XX 20-SEP-2000; 2000US-0234034P.

XX 20-SEP-2000; 2000US-0234052P.

XX 22-SEP-2000; 2000US-0234509P.

XX 22-SEP-2000; 2000US-0234567P.

XX 25-SEP-2000; 2000US-0234923P.

XX 25-SEP-2000; 2000US-0234924P.

XX 25-SEP-2000; 2000US-0235077P.

XX 25-SEP-2000; 2000US-0235082P.

XX 25-SEP-2000; 2000US-0235134P.

XX 26-SEP-2000; 2000US-0235280P.

XX 26-SEP-2000; 2000US-0235637P.

XX 26-SEP-2000; 2000US-0235638P.

XX 27-SEP-2000; 2000US-0235711P.

XX 27-SEP-2000; 2000US-0235720P.

XX 27-SEP-2000; 2000US-0235840P.

XX 28-SEP-2000; 2000US-0235863P.

XX 28-SEP-2000; 2000US-0236028P.

XX 28-SEP-2000; 2000US-0236032P.

XX 28-SEP-2000; 2000US-0236033P.

XX 28-SEP-2000; 2000US-0236034P.

XX 28-SEP-2000; 2000US-0236109P.

XX 28-SEP-2000; 2000US-0236111P.

XX 29-SEP-2000; 2000US-0236842P.

XX 29-SEP-2000; 2000US-0236891P.

XX 02-OCT-2000; 2000US-0237172P.

XX 02-OCT-2000; 2000US-0237173P.

XX 02-OCT-2000; 2000US-0237278P.

XX 02-OCT-2000; 2000US-0237294P.

XX 02-OCT-2000; 2000US-0237295P.

XX 02-OCT-2000; 2000US-0237316P.

XX 03-OCT-2000; 2000US-0237425P.

XX 03-OCT-2000; 2000US-0237598P.

XX 03-OCT-2000; 2000US-0237604P.

XX 03-OCT-2000; 2000US-0237606P.

XX 03-OCT-2000; 2000US-0237608P.

XX 01-NOV-2000; 2000US-0244867P.

XX 01-NOV-2000; 2000US-0245084P.

XX (AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

XX Soppet DR, Weaver Z;

XX WPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a chemical

XX agent to be tested for anti-neoplastic activity, and determining a change

XX in expression of a gene of a signature gene set.

XX Claim 1; SEQ ID NO 4660; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-

XX neoplastic agent. The method involves exposing cells to a chemical agent

XX to be tested for anti-neoplastic activity, determining a change in

XX expression of at least one gene (I) of a signature gene set, where (I)

XX comprises a sequence (S) selected from 8447 sequences (given in ABL61664

XX to ABL70110), or is at least 95% identical to (S), where a change in

XX expression is indicative of anti-neoplastic activity. (I) has cytostatic

CC activity and can be used in gene therapy. M1 can be used for screening an  
 CC anti-neoplastic agent, and can be used for producing a product which is  
 CC the data collected with respect to the anti-neoplastic agent as a result  
 CC of M1, and the data is sufficient to convey the chemical structure and/or  
 CC properties of the agent. M1 can be used in the treatment of cancer such  
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma, and Wilms  
 CC tumour

XX Sequence 528 BP; 147 A; 114 C; 156 G; 111 T; 0 U; 0 Other;

Query Match 96.9%; Score 522.2; DB 6; Length 528;  
 Best Local Similarity 99.4%; Pred. No. 7.5e-137;  
 Matches 524; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCAGGGAGCTGTGAGGCACTGCTGTGTGTTCTCCGCTCCGACTCTTTTTCCTCTAC 60

Db 2 GCCAGGGAGCTGTGAGGCACTGCTGTGTGTTCTCCGCTCCGACTCTTTTTCCTCTAC 61

QY 61 TGAGATTTCATCTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 120

Db 62 TGAGATTTCATCTGTGTAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 121

QY 121 CCAAGCGCTATTGTACAGCTCTCTGAAGTCATTTGGGCTATGCGGCCGAGCAGTTTCAGT 180

Db 122 CCAAGCGCTATTGTACAGCTCTCTGAAGTCATTTGGGCTATGCGGCCGAGCAGTTTCAGT 181

QY 181 GATGAAGTGGAAACACAGCAACACCTGGAAGAGGGGAAACCACTCAAGCTCAGGATCCT 240

Db 182 GATGAAGTGGAAACACAGCAACACCTGGAAGAGGGGAAACCACTCAAGCTCAGGATCCT 241

QY 241 GCAGCTGCTCAGGAGGAGGATGAGGAGGATCTGCGAGTCAAGGCGCGAAGCCTGAA 300

Db 242 GCAGCTGCTCAGGAGGAGGATGAGGAGGATCTGCGAGTCAAGGCGCGAAGCCTGAA 301

QY 301 GCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTCAAGATGGTCTGTAT 360

Db 302 GCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTCAAGATGGTCTGTAT 361

QY 361 GGGCAGGAGGTGGACCCGCAATCCAGAGGAGTGAAGAACGCTTGAAGAGTGAAGAG 420

Db 362 GGGCAGGAGGTGGACCCGCAATCCAGAGGAGTGAAGAACGCTTGAAGAGTGAAGAG 421

QY 421 CAATCACAGTGTAAAGAAAGACACGTTGAAATGATGCGGCTGCTCTATGTTGGAAT 480

Db 422 CAATCACAGTGTAAAGAAAGACACGTTGAAATGATGCGGCTGCTCTATGTTGGAAT 481

QY 481 TTGTTTCATTAAATTTCTCCCAATAAGCTTTACAGCCTTCTCAAAA 527

Db 482 TTGTTTCATTAAATTTCTCCCAATAAGCTTTACAGCCTTCTCAAAA 528

RESULT 6

AAV18720

ID AAV18720 standard; cDNA; 532 BP.

XX

AC AAV18720;

XX

XX

DT 30-JUL-1998 (first entry)

DE cDNA encoding GAGE-5 tumour rejection antigen precursor.

XX GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;

KW melanoma; antigen; cytolytic T cell clone proliferation;

KW HLA-typing assay; ss.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

75..429

/\*tag= a

FT

FT /transl\_except= (pos:189..191, aa:Ala)

XX /transl\_except= (pos:192..194, aa:Thr)

PN W09749417-A1.

XX 31-DEC-1997.

PD

XX

XX

PF 23-JUN-1997; 97WO-US010850.

XX

XX 24-JUN-1996; 96US-00669161.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

XX

PI Debacker O, Van Den Eynde B, Boon-Falleur T;

XX

DR WPI; 1998-076905/07.

DR P-PSDB; AAW47602.

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Db 361 AGATGACCGCGCCAAATCCAGAGGAGGTGAAAAACGCTGAAGAAGGTGAAAGCAATCAC 420  
QY 428 AGTGTAAAGAAACACACAGTTGAAATGATGCAGGCTGCTCTATGTTGGAAATTTGTTCA 487  
Db 421 AGTGTAAAGAAAGGACGTTGAAATGATGCAGGCTGCTCTATGTTGGAAATTTGTTCA 480  
QY 488 TTAATAATTCCTCCCAATAAAGCTTTACAGCCCTTCTGCAAAAAAATAAAAAA 539  
Db 481 TTAATAATTCCTCCCAATAAAGCTTTACAGCCCTTCTGCAAAAAAATAAAAAA 532  
  
RESULT 7  
AA90519  
ID AAX90519 standard; cdna; 538 BP.  
XX  
AC AAX90519;  
XX  
XX 30-SEP-1999 (first entry)  
DE GAGE-2 tumour rejection antigen clone nucleotide sequence.  
XX  
XX Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;  
KW therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;  
KW GAGE; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO937665-A1.  
XX  
XX 29-JUL-1999.  
XX  
XX 12-JAN-1999; 99WO-US000775.  
XX  
XX 23-JAN-1998; 98US-00012818.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX Van Der Bruggen P, Van Den Eynde B, Debacker O, Boon-Falleur T;  
PI WPT; 1999-469111/39.  
XX  
XX New isolated peptides which bind to HLA-A29 molecules, which are tumor  
PT rejection antigens used for detection and therapy of pathological  
PT conditions, e.g. cancer.  
XX  
XX Example 13; Fig 4; 62pp; English.  
XX  
XX The present invention describes peptides which bind to human leukocyte  
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into  
CC tumour rejection antigens. They can be used for detecting cytolytic T  
CC lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-  
CC typing assays. Complexes of HLA-29 molecules and the peptides can be used  
CC for stimulating CTLs in vivo. The present sequence represents a GAGE  
CC tumour rejection antigen clone, from an example from the present  
XX invention  
XX  
SQ Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;  
  
Query Match 94.7%; Score 510.2; DB 2; Length 538;  
Best Local Similarity 98.0%; Pred. No. 1.8e-133;  
Matches 528; Conservative 0; Mismatches 8; Indels 3; Gaps 1;  
  
QY 1 GCCAGGAGCTGTGTAGGAGCTGTGTGTGTCTTCCTGCGCTCGGACTCTTTTCTCTAC 60  
Db 3 GCCAGGAGCTGTAGGAGCTGTGTGTGTCTTCCTGCGCTCGGACTCTTTTCTCTAC 62  
QY 61 TGAGATTCATCTGTGTGAATATGATTTGGGAGAGATCGACCTATTATGGCCTAGA 120  
Db 63 TGAGATTCATCTGTGTGAATATGATTTGGGAGAGATCGACC--TATCGGCCTAGA 119  
QY 121 CCAAGGCGCTATGTACAGCTCTCTCAAGTGTGTTGGGCTATGCGGCGGAGCAGTTCAGT 180  
Db 120 CCAAGACCTACGTAGAGCTCTCTGAATGATTTGGGCTATGCGGCGGAGCAGTTCAGT 179

RESULT 8

ADAL5802

ID ADAL5802 standard; cdna; 526 BP.

XX AC ADAL5802;

XX DT 06-NOV-2003 (first entry)

XX DE Human GAGE-7B cdna.

XX KW Human; GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL;

KW human leukocyte antigen; HLA; tumour rejection antigen precursor;

KW major histocompatibility complex; MHC; cytolytic T cell proliferation;

XX KW chromosome Xp11.2-p11.4.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 55..408

FT FT /\*tag= a

FT FT /product= "Human GAGE-7B"

FT FT /transl\_except= (pos:115..162, aa: GPMRPEQGSDEVPEMI)

FT FT /transl\_except= (pos:265..306, aa: HPQIGKPEAHSEQE)

XX US6509172-B1.

XX PD 21-JAN-2003.

XX PF 30-SEP-1998; 98US-00163748.

XX PR 30-SEP-1998; 98US-00163748.

XX (LUDW-) LUDWIG INST CANCER RES.

XX De Backer O, Van Den Eynde B, Boon-Falleur T;

XX WPI; 2003-401119/38.

XX P-PSDB; ADA15777.

XX New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor

PT rejection antigen precursors, which complex to major histocompatibility

PT complex molecules to facilitate the proliferation of cytolytic T cells.

XX Claim 1; Col 9-10; 15pp; English.

XX The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the

CC nucleic acid molecules encoding them. The invention also relates to an

CC expression vector comprising an isolated nucleic acid molecule of the  
CC invention operably linked to a promoter, a recombinant cell comprising  
CC the isolated nucleic acid molecule or the expression vector and an  
CC expression kit useful in generating cytolytic T lymphocytes (CTLs) or  
CC determining if CTLs are present in a sample comprising the isolated  
CC nucleic acid molecule and the isolated nucleic acid that encodes a human  
CC leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid  
CC molecules encode tumour rejection antigen precursors, which complex to  
CC major histocompatibility complex (MHC) molecules to facilitate the  
CC proliferation of cytolytic T cells. This sequence represents cDNA  
CC encoding the human GAGE-7B polypeptide of the invention. The gene resides  
CC on chromosome Xp11.2-p11.4.  
XX  
SQ Sequence 526 BP; 168 A; 109 C; 143 G; 106 T; 0 U; 0 Other;

Query Match 93.5%; Score 504; DB 7; Length 526;  
Best Local Similarity 99.0%; Pred. No. 1e-131;  
Matches 507; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 28 TGGTTCTGCGCTCGGACTCTTTTCTCTACTGAGATTCTCTGTGAATATGAGT 87  
Db 1 TGGTTCTGCGCTCGGACTCTTTTCTCTACTGAGATTCTCTGTGAATATGAGT 60  
QY 88 TGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCGAA 147  
Db 61 TGGCGAGGAAGATGACCTATTATTGGCTAGACCAAGCGCTATGTACAGCTCTCGAA 120  
QY 148 GTGATGGGCTATGCGGCCGAGCAGTTCAGTATGATGAAGTGGAAACCACTGAA 207  
Db 121 ATGATTTGGGCTATGCGGCCGAGCAGTTCAGTATGATGAAGTGGAAACCACTGAA 180  
QY 208 GAAGGGGAACCAAGCACTCAAGTTCAGGATCTGCGAGTCTCAGAGGGAGAGATGAG 267  
Db 191 GAAGGGGAACCAAGCACTCAAGTTCAGGATCTGCGAGTCTCAGAGGGAGAGATGAG 240  
QY 268 GGAGCATCTGCAAGGTCAAGGGCCGAGCTGAAGCTGATAGCCAGGAACAGGGTCACCCA 327  
Db 241 GGAGCATCTGCAAGGTCAAGGGCCGAGCTGAAGCTCATAGCCAGGAACAGGGTCACCCA 300  
QY 328 CAGACTGGGTGTGATGTGAAGATGGTCTGTATGGGCGAGGAGTGGACCCGCAATCCA 387  
Db 301 CAGACTGGGTGTGATGTGAAGATGGTCTGTATGGGCGAGGAGTGGACCCGCAATCCA 360  
QY 388 GAGGAGGTGAACCCCTGGAAGAGGTGAAGAGCAATCACAGTGTAAAGAGACAGT 447  
Db 361 GAGGAGGTGAACCCCTGGAAGAGGTGAAGAGCAATCACAGTGTAAAGAGACAGT 420  
QY 448 TGAATGATGCAAGGCTGCTCCTATTTTGGAAATTTTGTTCATTAAATTTCTCCCAATAAG 507  
Db 421 TGAATGATGCAAGGCTGCTCCTATTTTGGAAATTTTGTTCATTAAATTTCTCCCAATAAG 480  
QY 508 CTTTACAGCTTCTGCAAAAAAATAAAAAA 539  
Db 481 CTTTACAGCTTCTGCAAAAAAATAAAAAA 512

RESULT 9  
ADA15801  
ID ADA15801 standard; cDNA; 528 BP.  
XX  
AC ADA15801;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human GAGE-8 cDNA.  
XX  
KW Human; GAGE-8; gene; ss; cytolytic T lymphocyte; CTL;  
KW human leukocyte antigen; HLA; tumour rejection antigen precursor;  
KW major histocompatibility complex; MHC; cytolytic T cell proliferation;  
XX chromosome Xp11.2-p11.4.  
OS  
XX Homo sapiens.

PH Key Location/Qualifiers  
FT CDS 73..423  
FT /\*tag= a  
FT /product= "Human GAGE-8"  
FT /transl\_except= (pos:244..246, aa:Gln)  
FT /transl\_except= (pos:400..402, aa:Lys)  
XX  
FN US6509172-B1.  
XX  
XX  
PD 21-JAN-2003.  
XX  
XX 30-SEP-1998; 98US-00163748.  
XX  
PR 30-SEP-1998; 98US-00163748.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI De Backer O, Van Den Bynde B, Boon-Falleur T;  
XX  
DR WPI, 2003-401119/38.  
DR P-PSDB; ADA15778.  
XX  
PT New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor  
PT rejection antigen precursors, which complex to major histocompatibility  
PT complex molecules to facilitate the proliferation of cytolytic T cells.  
XX  
PS Claim 1; Col 7-10; 15pp; English.  
XX  
CC The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the  
CC nucleic acid molecules encoding them. The invention also relates to an  
CC expression vector comprising an isolated nucleic acid molecule of the  
CC invention operably linked to a promoter, a recombinant cell comprising  
CC the isolated nucleic acid molecule or the expression vector and an  
CC expression kit useful in generating cytolytic T lymphocytes (CTLs) or  
CC determining if CTLs are present in a sample comprising the isolated  
CC nucleic acid molecule and the isolated nucleic acid that encodes a human  
CC leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid  
CC molecules encode tumour rejection antigen precursors, which complex to  
CC major histocompatibility complex (MHC) molecules to facilitate the  
CC proliferation of cytolytic T cells. This sequence represents cDNA  
CC encoding the human GAGE-8 polypeptide of the invention. The gene resides  
CC on chromosome Xp11.2-p11.4.  
XX  
SQ Sequence 528 BP; 158 A; 112 C; 151 G; 107 T; 0 U; 0 Other;

Query Match 93.3%; Score 502.8; DB 7; Length 528;  
Best Local Similarity 98.1%; Pred. No. 2.2e-131;  
Matches 520; Conservative 0; Mismatches 7; Indels 3; Gaps 1;  
QY 10 CTGTGAGGCACTGTGTGTGTTCTCTGCGCTCGGACTCTTTTCTCTACTGAGATTCA 69  
Db 1 CTGTGAGGCACTGTGTGTGTTCTCTGCGCTCGGACTCTTTTCTCTACTGAGATTCA 60  
QY 70 TCTGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCCCTAGACCAAGCGC 129  
Db 61 TCTGTGTGAATATGAGTTGGCGAGGAGATCGACCTATTATTGGCCCTAGACCAAGCGC 117  
QY 130 TATGTACAGCTCTCTGAAGTCAATTGGGCTATGCGGCCGAGAGTTCAGTGAAGATG 189  
Db 118 TACGTAGAGCTCTCTGAAGTCAATTGGGCTATGCGGCCGAGAGTTCAGTGAAGATG 177  
QY 190 GAACCAACACCTGAGAGAGGGGMAACCACTCAACCTCAGGATCCTGCAGCTCT 249  
Db 178 GAACCAACACCTGAGAGAGGGGMAACCACTCAACCTCAGGATCCTGCAGCTCT 237  
QY 250 CAGGAGGAGAGGATGAGGAGGATCTGAGGTCAAGGCGCAAGCCCTGAAGCTGATAGC 309  
Db 238 CAGGAGGAGAGGATGAGGAGGATCTGAGGTCAAGGCGCAAGCCCTGAAGCTGATAGC 297  
QY 310 CAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTGGCAGGAG 369  
Db 298 CAGGAACAGGGTCAACCCACAGACTGGGTGTGAGTGTGAAGATGGTCTGTGGCAGGAG 357

QY 370 GTGGACCCGCCAAATCCAGAGGAGTGAAAAACCCCTGAAGAGGTGAAAAGCAATCACAG 429  
 Db 358 ATGGACCCGCCAAATCCAGAGGAGTGAAAACCCCTGAAGAGGTGAAAAGCAATCACAG 417  
 QY 430 TGTAAAGAGACACAGTTGAAATGATGAGGAGTGTCTTATGTTGAAATTTGTTCAAT 489  
 Db 418 TGTAAAGAGACACAGTTGAAATGATGAGGAGTGTCTTATGTTGAAATTTGTTCAAT 477  
 QY 490 AAAATTCTCCCAATAAGCTTTACAGCCTTCTGCAAAAAAAGAAAAA 539  
 Db 478 AAAATTCTCCCAATAAGCTTTACAGCCTTCTGCAAAAAAAGAAAAA 527

RESULT 10  
 ID ABZ20463  
 AC ABZ20463;  
 XX 23-JAN-2003 (first entry)  
 DE GAGE-2 full length cDNA sequence SEQ ID NO:2890.  
 XX Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
 KW immune response; virology; immunology; microbiology; molecular biology;  
 KW recombinant DNA technology; gene; ss.  
 XX Homo sapiens.  
 XX WO200278516-A2.  
 FN 10-OCT-2002.  
 PD 28-MAR-2002; 2002WO-US010421.  
 XX 30-MAR-2001; 2001US-0280255P.  
 PR 28-AUG-2001; 2001US-0315563P.  
 PR 09-JAN-2002; 2002US-0347313P.  
 XX (CORI-) CORIXA CORP.  
 PA Wang T, Wang S, Bangur CS, Gaiger A;  
 XX WPI; 2003-058387/05.  
 DR P-PSDB; ABP54447.  
 XX New immunogenic polynucleotides or polypeptides useful for diagnosing,  
 PT preventing and treating cancer expressing CT or Cp mRNA antigens, and in  
 PT virology, immunology, microbiology, molecular biology and recombinant DNA  
 PT techniques.  
 XX Claim 1; SEQ ID NO 2890; 207pp; English.  
 PS ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
 XX ABP54446 to ABP54472 represent protein (II) sequences, from the present  
 CC invention. (I) and (II) have cytostatic activity and can be used in gene  
 CC therapy and vaccines. (I), (II), antibodies and compositions from the  
 CC present invention are useful for diagnosing, preventing and treating  
 CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
 CC stimulating immune response. They can also be useful in virology,  
 CC immunology, microbiology, molecular biology and recombinant DNA  
 CC techniques. N.B. The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 530 BP; 152 A; 116 C; 155 G; 107 T; 0 U; 0 Other;  
 SQ

Query Match 93.2%; Score 502.2; DB 7; Length 530;  
 Best Local Similarity 97.9%; Pred. No. 3.3e-131;  
 Matches 520; Conservative 0; Mismatches 8; Indels 3; Gaps 1;  
 QY 1 GCACGGAGCTGAGCAGTGTGTGTCTCTCGGACTCTTTCTCTCTAC 60  
 |||

Db 3 GCACGGAGCTGAGCAGTGTGTGTCTCTCGGACTCTTTCTCTCTCTAC 62  
 QY 61 TCAGATTTCATCTGTGTGAAATATAGTTGGCAGGAGATCGACCTATTATTATGGCCCTAGA 120  
 Db 63 TGAGATTTCATCTGTGTGAAATATAGTTGGCAGGAGATCGACCTATTATTATGGCCCTAGA 119  
 QY 121 CCAAGGCGCTATGTACAGCCTCTCTGAAGTGATTGGGCTTATGGGCCCGCAGCAGTTTCAGT 180  
 Db 120 CCAAGGCGCTATGTACAGCCTCTCTGAAGTGATTGGGCTTATGGGCCCGCAGCAGTTTCAGT 179  
 QY 181 GATGAAGTGGAAACCAAGCAACACCTGAAGAAAGGGAACCAAGCAACCTCAAGTCAGGATTCCT 240  
 Db 180 GATGAAGTGGAAACCAAGCAACACCTGAAGAAAGGGAACCAAGCAACCTCAAGTCAGGATTCCT 239  
 QY 241 GCAGCTGTCTCAGGAGGAGGAGGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAA 300  
 Db 240 GCAGCTGTCTCAGGAGGAGGAGGAGGAGCATCTGCAGGTCAAGGGCCGAGGCTGAA 299  
 QY 301 GCTGATAGCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCCTGAT 360  
 Db 300 GCTGATAGCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGTCCTGAT 359  
 QY 361 GGGCAGGAGGTGACCCGCCAAATCCAGAGGAGGTGAAAACGGCTGAAAGGTGAAAAG 420  
 Db 360 GGGCAGGAGGTGACCCGCCAAATCCAGAGGAGGTGAAAACGGCTGAAAGGTGAAAAG 419  
 QY 421 CAATCACAGTGTAAAGAAAGACACGTTGAAATGATCAGGCTGCTCTATGTTGAAAT 480  
 Db 420 CAATCACAGTGTAAAGAAAGACACGTTGAAATGATCAGGCTGCTCTATGTTGAAAT 479  
 QY 481 TTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCCTTTGCAAAAAA 531  
 Db 480 TTGTTCAATTAATAATCTCCCAATAAGCTTTACAGCCTTTGCAAAAAA 530

RESULT 11  
 AAV18717  
 ID AAV18717 standard; cDNA; 535 BP.  
 XX AAV18717;  
 XX 30-JUL-1998 (first entry)  
 DE cDNA encoding GAGE-2 tumour rejection antigen precursor.  
 XX GAGE tumour rejection antigen precursor; TRAP; tumour; diagnosis;  
 KW melanoma; antigen; cytolytic T cell clone proliferation;  
 KW HLA-typing assay; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT CDS 81..431  
 FT /\*tag= a  
 FT /transl\_except= (pos:192..194, aa:Ala)  
 FT /transl\_except= (pos:195..197, aa:Thr)  
 XX WO9749417-A1.  
 XX 31-DEC-1997.  
 XX 23-JUN-1997; 97WO-US010850.  
 XX 24-JUN-1996; 96US-00669161.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX Debacker O, Van Den Eynde B, Boon-Falleur T;  
 XX WPI; 1998-076905/07.  
 DR P-PSDB; AAW47599.  
 XX Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -



processed by HLA-Cw6 molecules into peptides, useful to diagnose melanomas.

Example 13; Fig 4; 60pp; English.

The present sequence encodes a GAGE-2 tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE cDNAs for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants

Sequence 535 BP; 158 A; 112 C; 156 G; 109 T; 0 U; 0 Other;

Query Match 86.9%; Score 468.4; DB 2; Length 535;  
Best Local Similarity 95.6%; Pred. No. 1.1e-121;  
Matches 516; Conservative 0; Mismatches 16; Indels 8; Gaps 3;

```

QY 1 GCCAGGGAGCTGTGAGGAGTCTGTGTGGTTCCTGCCGTCGGACTCTTTTTCCTC-TA 59
DB 3 GCCAGGGAGCTGTGAGGAGTCTGTGTGGTTCCTGCCGTCGGACTCTTTTTCCTC-TA 58
QY 60 CTGAGATTCATCTGTGTGAATATGAGTTGGGAGGAGATGACACTATTATTGGCTAG 119
DB 59 CTGAGATTCATCTGTGTGAATATGAGTTGGGAGGAGATGACACTATTATTGGCTAG 115
QY 120 ACCAAGGGCTATGTACAGCTCTCTGAAGTATGGGCTATGCCGCCGAGCAGTTCTAG 179
DB 116 ACCAAGAGCTACGTAGAGCTCTCTGAATATGTTGGGCTATGCCGCCGAGCAGTTCTAG 175
QY 180 TGATGAAGTGAACCCAGCAGACCTCTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCC 239
DB 176 TGATGAAGTGAACCCAGCAGCTCTCTGAAGAGGGGAAACAGCAACTCAACGTCAGGATCC 235
QY 240 TGCAGCTGCTCAGGAGGAGAGGTGAGGAGCAGTCTGCAGGTCAAGGCCGAGACCTGA 299
DB 236 TGCAGCTGCTCAGGAGGAGAGGTGAGGAGCAGTCTGCAGGTCAAGGCCGAGACCTGA 295
QY 300 AGCTGATAGCCAGGAAACAGGGTCAACCCAGACTGGGTGTGAGTGTGAAGTGGTCTCTGA 359
DB 296 AGCTGAGAGCCAGGAAACAGGGTCAACCCAGACTGGGTGTGAGTGTGAAGTGGTCTCTGA 355
QY 360 TGGCAGAGGTGAGCCCGCCAAATCCAGAGAGGTGAAACCGCTGAGAGAGGTGAAAA 419
DB 356 TGGCAGAGAGTGAACCCCGCCAAATCCAGAGAGGTGAAACCGCTGAGAGAGGTGAAAA 415
QY 420 GCAATCAAGTGTAAAGACACACGTTGAATCATGACGAGCTCTCTCTATGTGGAAA 479
DB 416 GCAATCAAGTGTAAAGACACATGTTGAATCATGACGAGCTCTCTCTATGTGGAAA 475
QY 480 TTTGTTTCATTAATTTCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAAAGAAAAA 539
DB 476 TTTGTTTCATTAATTTCTCCCAATAAAGCTTTACAGCTTCTGCAAAAAAAGAAAAA 535

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RESULT 12

AAC02129

ID AAC02129 standard; cDNA; 430 BP.

XX

AC AAC02129;

XX

DT 06-OCT-2000 (first entry)

XX

DE Human secreted protein 5' EST, SEQ ID NO: 2127.  
XX  
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1033401-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 21-FEB-2000; 2000EP-00200610.  
XX  
PR 26-FEB-1999; 99US-0122487P.  
XX (GEST ) GENSET.  
PA  
PI Dumas Milne Edwards J, Duclert A, Giordano J;  
XX  
DR WPI; 2000-500381/45.  
DR P-PSDB; AAG02123.

XX  
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
XX  
PS Claim 1; SEQ ID NO 2127; 71pp + Sequence Listing; English.

XX The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. An ORF has been identified within the  
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
CC derived from 30 different tissues. EST sequences usually correspond  
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
CC well suited for isolating cDNA sequences derived from the 5' ends of  
CC mRNAs and even in those cases where longer cDNA sequences have been  
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
CC mRNAs with intact 5' ends and can therefore be used to obtain full length  
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
CC gene therapy and chromosome mapping procedures. They are used to obtain  
CC upstream regulatory sequences and to design expression and secretion  
CC vectors  
XX  
SQ Sequence 430 BP; 101 A; 102 C; 134 G; 85 T; 0 U; 8 Other;

Query Match 66.1%; Score 356.2; DB 3; Length 430;  
Best Local Similarity 97.3%; Pred. No. 4.1e-90;  
Matches 366; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

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QY 1 GCCAGGAGCTGTGAGGAGTCTGTGTGGTTCCTGCCGTCGGACTCTTTTTCCTCTAC 60
DB 56 GCCAGGAGCTGTGAGGAGTCTGTGTGGTTCCTGCCGTCGGACTCTTTTTCCTCTAC 115
QY 61 TGAGATTCATCTGTGTGAATATGAGTTGGGAGAGATGACCTATTATTGGCTAGA 120
DB 116 TGAGATTCATCTGTGTGAATATGAGTTGGGAGAGATGACCTATTATTATTGGCTAGA 174
QY 121 CCAAGGCGCTATGTACAGCTCTCTGAAGTGTGGGCTATGCCGCCGAGCAGTTCACT 180
DB 175 CCAAGGCGCTATGTACAGCTCTCTGAAGTGTGGGCTATGCCGCCGAGCAGTTCACT 234
QY 181 GATGAAGTGAACCCAGCAGACCTCTGAAGAGAGGAAACAGCAACTCAACGTCAGATCCT 240
DB 235 GATGAAGTGAACCCAGCAGACCTCTGAAGAGAGGAAACAGCAACTCAACGTCAGATCCT 294
QY 241 GCAGTGTCTCAGGAGGAGAGGATGAGGAGCAGTCTGCAGGTCAAGGCCGAGCCTGAA 300
DB 295 GCAGTGTCTCAGGAGGAGAGGATGAGGAGCAGTCTGCAGGTCAAGGCCGAGCCTGAA 354
QY 301 GCTGATAGCCAGGAAACAGGGTCAACCCAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 360
DB 355 GCTCATAGCCAGGAAACAGGGTCAACCCAGACTGGGTGTGAGTGTGAAGATGGTCTGAT 414

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CC protein. Cancers which may be targeted include carcinoma (e.g. squamous  
CC cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic  
CC leukaemia), lymphoma, plasmocytoma, reticulend cell sarcoma, Hodgkin's  
CC disease and tumours (e.g. glioma). The present sequence is one of the  
CC 1046 novel cancer cell markers  
XX  
SQ Sequence 365 BP; 63 A; 86 C; 66 G; 150 T; 0 U; 0 Other;

Query Match 55.8%; Score 300.8; DB 4; Length 365;  
Best Local Similarity 96.2%; Pred. No. 1.6e-74;  
Matches 308; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
QY 220 GCAACTCAACGTCAGACTCTGCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGCA 279  
Db |||||  
365 GCAACTCAACGTCAGACTCTGCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGCA 306  
QY 280 GGTCAAGGGCCGAAAGCCCTGAAAGCTGATAGCCAGGAAACAGGGTCAACCCACAGACTGGGTGT 339  
Db |||||  
305 GGTCAAGGGCCGAAAGCCCTGAAAGCTGATAGCCAGGAAACAGGGTCAACCCACAGACTGGGTGT 246  
QY 340 GAGTGTGAAGATGCTCTGATGGGCGAGGAGTGGACCCGCAATTCAGAGAGGTGAAA 399  
Db |||||  
245 GAGTGTGAAGATGCTCTGATGGGCGAGGAGTGGACCCGCAATTCAGAGAGGTGAAA 186  
QY 400 ACGCTGAAAGAGGTGAAAAGCAATCACAGTGTGTTAAAAAGAGACACGTTGAAATGATGCA 459  
Db |||||  
195 ACGCTGAAAGAGGTGAAAAGCAATTCAGTGTGTTAAAAAGGACGTTGAAATGATGCA 126  
QY 460 GGCTGCTCCTATGTTGGAAAATTGTTCAATTAATAATTCCTCCCAATAAAGCTTTACAGCCTT 519  
Db |||||  
125 GGCTGCTCCTATGTTGGAAAATTGTTCAATTAATAATTCCTCCCAATAAAGCTTTACAGCCTT 66  
QY 520 CTGCAAAAAAATAAAAAA 539  
Db 65 CTAAAAAATAAAAAA 46

## RESULT 15

ABZ19551/C  
ID ABZ19551 standard; cDNA; 277 BP.

XX AC ABZ19551;

XX DT 23-JAN-2003 (first entry)

XX DE Group III cDNA cancer related clone SEQ ID NO:1977.

XX KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
KW immune response; virology; immunology; microbiology; molecular biology;  
KW recombinant DNA technology; gene; ss.

XX OS Homo sapiens.

XX FN WO200278516-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US010421.

XX PR 30-MAR-2001; 2001US-0280255P.

XX PR 28-AUG-2001; 2001US-0315563P.

XX PR 09-JAN-2002; 2002US-0347313P.

XX PA (CORI-) CORIXA CORP.

XX PI Wang T, Wang S, Bangur CS, Gaiger A;

XX DR WPI; 2003-058387/05.

XX PT New immunogenic polynucleotides or polypeptides useful for diagnosing,  
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
PT virology, immunology, microbiology, molecular biology and recombinant DNA  
PT techniques.

XX PS Claim 1; SEQ ID NO 1977; 207pp; English.

XX ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
CC invention. (I) and (II) have cytostatic activity and can be used in gene  
CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques. N.B. The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 277 BP; 62 A; 79 C; 73 G; 63 T; 0 U; 0 Other;

Query Match 45.3%; Score 244; DB 7; Length 277;

Best Local Similarity 100.0%; Pred. No. 1.4e-59;

Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGGAGCTGTGAGGAGTGTGTTGTTCTCGGCTCGGACTCTTTTCTCTAC 60

Db |||||  
244 GCCAGGGAGCTGTGAGGAGTGTGTTGTTCTCGGCTCGGACTCTTTTCTCTAC 185

QY 61 TGAGATTTCATCTGTGTAATATGAGTTGGCGAGAGATCGACCTATTATGGCCTAGA 120

Db |||||  
194 TGAGATTTCATCTGTGTAATATGAGTTGGCGAGAGATCGACCTATTATGGCCTAGA 125

QY 121 CCAAGGCGCTATGTACAGCCTCTGAGTGTGTTGGGCTATGCGGCCGAGCAGTTCACT 180

Db |||||  
124 CCAAGGCGCTATGTACAGCCTCTGAGTGTGTTGGGCTATGCGGCCGAGCAGTTCACT 65

QY 181 GATCAAGTGGAAACGAGCAACACCTGAAAGAGGGGAAACGAGCAACTCAACGTCAGATCCT 240

Db |||||  
64 GATCAAGTGGAAACGAGCAACACCTGAAAGAGGGGAAACGAGCAACTCAACGTCAGATCCT 5

QY 241 GCAG 244

Db |||||  
4 GCAG 1

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